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TTGAAGGCAG CCAGATCTGT TAAACTCTGT CCTTTCCCTC TCCGGAAGAG CAGCATGAAG
CTGGCATTCC TCTTCCTTGG CCCCATGGCC CTCCTCCTTC TGGCTGGCTA TGGCTGTGTC
CTCGGTGCCT CCAGTGGGAA CCTGCGCACC TTTGTGGGCT GTGCCGTGAG GGAGTTTACT
TTCCTGGCCA AGAAGCCAGG CTGCAGGGGC CTTCGGATCA CCACGGATGC CTGCTGGGGT
CGCTGTGAGA CCTGGGAGAA ACCCATTCTG GAACCCCCCT ATATTGAAGC CCATCATCGA
GTCTGTACCT ACAACGAGAC CAAACAGGTG ACTGTCAAGC TGCCCAACTG TGCCCCGGGA
GTCGACCCCT TCTACACCTA TCCCGTGGCC ATCCGCTGTG ACTGCGGAGC CTGCTCCACT
GCCACCACGG AGTGTGAGAC CATCTGA (SEQ ID NO: 1)

ATGAACAAGA AGAGGGTGAT GTTCCCTGTC CTGCAGCTTC TGGTTTTAGC CCTGTGTCTC
AGCACCGCTG CAGGATCCAA TATAAGTCTG AGAACGTTCA TTGGATGTGC TGTGAGGGAA
TTCACATTCT TAGCAAAGAA ACCTGGCTGC AGAGGTCTGC GTGTGACTAC TGATGCCTGC
TGGGGGCGCT GTGAGACCTG TGAGAAGCCA TCCCTAGATC CTCCGTACAT AGAAGCCCAC
CACAGAGTCT GCACTTACAA TGAAACTAAA CTGGTTACTG TAATACTGCC AAACTGCAGC
CCAGACATTG ACCCATTCTT TACCTACCCA GTTGCCATTA GATGTGACTG TGACATGTGG
TCCACTTCTA CTACAGAATG T (SEQ ID NO: 3)

FIG.1

MKLAFLLLGP MALLLLAGYG CLGASSGNLR TFVGCAVREF TFLAKKPGCR
GLRITTDACW GRCETWEKPI LEPPYIEAHH RVCTYNETKQ VTVKLPNCAP
GVDPFYTYPV AIRCDCGACS TATTECETI (SEQ ID NO: 2)

MNKKRVKFPV LQLLVLALCL STAAGSNISL RTFIGCAVRE FTFLAKKPGC
RGLRVTTDAC WGRCETCEKP SLDPPYIEAH HRVCTYNETK LVTVILLPNC
SPDIDPFFTY PVAIRCDCMW STSTTEC (SEQ ID NO: 4)

FIG. 2

MKLAFLLLGPMALLLLAGYGCLG (SEQ ID NO: 10)

FIG. 3

```
aggaatctct ggatgcctgt gttggagttt gtgggcattt acaatttctg ggctcatttt
ccctgaaatg ctaggagcaa ggtccctttg atagtgacaa atgcatggtt ggctgtgcca
ttgaaggcag ccagatctgt taaactctgt cctttccctc tccggaagag cagcatgaag
                                                          M  K

ctggcattcc tcttccttgg ccccatggcc ctcctccttc tggctggcta tggctgtgtc
 L  A  F   L  L  L  G   P  M  A   L  L  L   L  A  G  Y   G  C

ctcggtgcct ccagtgggaa cctgcgcacc tttgtgggct gtgccgtgag ggagtttact
 L  G  A   S  S  G  N   L  R  T   F  V  G   C  A  V  R   E  F  T

ttcctggcca agaagccagg ctgcaggggc cttcggatca ccacggatgc ctgctggggt
 F  L  A   K  K  P  G   C  R  G   L  R  I   T  T  D  A   C  W  G

cgctgtgaga cctgggaggt gagttgctaa gttgtgcaga tgacagtgtc ttctaggcca
 R  C  E   T  W  E < intron ----------------

gcagcttggg tctgattctt aagagttcac tttttaaatg atatgaggta gagctgggac
atctgccctt tcctgtggac ttaaaaaacc aaaacaaaac tatgattggc atcttccaaa
agtgatttga aaaacatgat gttgcccctc taacaaagca ttgataaggt taagaatttg
gtttacattg tgtctatgta tctgggaatc atctctggga ggtcaagatg tactgttcta
cccgttttac agatgacatg gagggattca agggagagtg gctgcaaagt cacgtagagc
gtcagtgtaa agctgggaat caatctgtgg ttcaagcttg tgacccaaac tcctccctat
gtttcctcat tttggataaa ttagccagtt tccaagaaag aggccctgag ctgaagggtg
agcgttggtc ccagtgaagg gtgagacccc ttcactgcct cttctgcagc ccttttcctc
ctcaagtctc tgggagccct ctggggttat cactgacgga tccattaagt tccttcatat
tcaattatac ctggcctttt tagagacatt taatttaaag tggagataac actctcaaac
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gtctgcctgc tttcctggag acagcacatt ttcttactct ggccttggta agtgactttc
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ccttcccatc tgtcattatc atatttattc ctgatgccta tctgcagtgc cagctccctt
tctgggcctt ttttgacttg caggtaagcc cttgactatg ctctactttt cgtcttactt
cctcccccac cacacgcgtg atttaaattt tttcaggaca gaggttcatt cttataacct
tcacagcttt tgtcaagatg tcgtgtatga acaaggcatt caatacacat ttgttggttg
actgggatgg acctcccccc ggagctgtag atcctccagc ctaatggaag gccatttaga
atcacacttg cactgtgagt ggacactgcc attgggaaaa atagccttct ctttggggac
ccagagggta acctgctctt gcttaggtac aattacggcc ctgtgaatgg aattgggtca
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ctgtcaattg gcagcaaatt cacctggggc acttggcacc tcctcctgtt cagggactgg
cctggcaggg cctctccctg ttcgcatcta gtgtctgggc tatttgaagc cctctctgtg
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tgatgaatgt ctttaattgg atcatggtca cccataggag gtcaggaact gtgctctcac
tggaaagatg gaaacaccaa aaccgttaaa gaacaagatt ctccctgatg ttagccagct
ttcattcatg tcttgactgt gttatgaaaa gggaggttac ctatagaaaa taaataaaag
aatgagattc attttcccag caatctgaaa gtttctgcgc tataaagcac ttgatttttt
ggtgggggggg atcttaactg aaagcatgtc tgaaaataag gatgttcatg atgacaggct
ggctggattt acatttgaag gttgttgaaa atagctattc ctcataatct gggtatagag
ttgccagatt tagcaaacaa acaaacagac aaacaaaata aaacaaaacc aatcccctcc
ccacagaaac ccaaactgaa ataaaaccag aaaaccagga agcccaggta aattggaatt
taagataaat aataaataaa tttttagcgt aagtctgtct gtctcataca gtatttggga
tgacttatac taaaaaatta tgtatctgaa aatgaaattt tacggggcgt ttggtctgcc
taggttccca gagtactaat ggtaagagga cttaaagcaa atacgggaag gtaggagaaa
```

FIG. 4

```
acagttcagg acaaattcag ctcttctggt ctttgtcaaa ggcaaggctg gccgggcgtg
gtggctaaca cctgtaatct cagcactttg ggaggctgtg gtgggtggat aatgaggtca
ggagttcgag accagcctgg ccagttttta gtaaagaggt gagttaaacc ctgtctctac
taaaaataca aaaattagcc gggcatggtg gtatgcacct gtagtcccag ctacttggga
ggctgaggca gaagacttgc ttgaacccag gaggtggagg ttacagtgag ccaagatcat
gccactatac tccagcctgg cgacagagtg agactccatc tcaaaaaaaa aaaaaaaaga
aaaaagaaaa aaaaaaggta aggctgctat tttcatgaca ttcatgcaag aacatcttga
gttacatatg tatatatatt ctttttgcc tagaacaaag aagaaccaaa aagcaaaggt
actgtcattt gaaagcttgt tattatttac attactttct tataataatt gcactaataa
gaacaatgga ttggctgggc gtggtggctc acgcctgtaa tcccagcact ttgggaggcc
gaggcaggca gatcacgagg tcaggaaatc gagaccatcc tggctaacat ggtgaaaccc
tgtctctact aaaaatacaa aaaatgagcc aggcgtggtg gtgggtgcct gtagtcccgg
gaggctgagg caggagaatg gcgtgaaccc gggaggcgga gattgcaatg agctgagatt
gcgccactga actccagcct gggagacagc aagactccgt ctcaaaaaaa aaaaaaatgg
attgcatttt ttgaacattt actttgttct agacattgtg cattgcgtat atcatcttac
cttatctctc aaacaatggt gggaggtagc tattttgttt tacagaggag gaaacttgag
tcttcaggaa gttaagtgga ttttccaagg tctccagcaa gtggcagaac agggactcaa
gctccttagt tctgactgca gggctcgaga ttttaactcc agctaggtgc tgatattttt
tctgatctgt gtgttctgtt tatcaaaatt gtctttgaac ttaagattta taaaaggtga
aggaaggaaa tgaatctttt tgatgatcag aacagtgcac agagtattcg ggaacctgtc
ttgtaatgtt ttctttcatt gattcaatga caaatagtta ttgaaactct cccggggtct
gttttgggta cttgaggcac agtgggcaaa aatctctgtc ctaaaagagc ttactttcta
gagtgggagg aatatcacac gaatgaaagg tagactacgt cgtgtggtat tgatcagtgc
tgtggtggaa aataaagcaa gatgggggat gggaagtttc tgggcatgga gatggaatgt
tgcaatttta aataggatgg tcaggaaatg cttccctgag agggtgacat tctaacaaaa
acccaaggtt ggtgaaagag tgaatcatac gggagaagaa tgttccaggc agaaggaacg
gtaagtgcaa aggccctgag ctggggctgt tcctggtggg tcagaggagc aataaggaga
ccgccgtgag cctagtgagg aagtcagtga ggtgggaatg gttgcaggca tttcagaagg
tagagttgca gagaaggtga tgtaggtctt gaaggtgatc ataaggtctt tgatgtttgt
tctgagtgag atgggaaatc actggggctt tgggcagagg agtgacatga tctgacttag
gtttaaacag gatcactcag ggccgctgtg ttgcaaatag attgtaggga gtaaaaatgg
aagaggggag accagttaga aggtatttgc aatgactaag atgattcatt tgctgactat
gcatggagca cttgctgtgt gctatggtct ctcctgggag cttagaatat ggtcttgagt
gaaatcagct tcttgctttc aggagtttgt tttctactgg gagacgacag agcaacaagt
aaatcaacga ataacaagtt aatttctgat agtgataaat gatactaaaa aactgaaaca
agatcatatg ttctaatgaa ttctctgttt tctatctatg gggacagaaa cccattctgg
                                    end of intron > K   P  I  L

aacccccta tattgaagcc catcatcgag tctgtaccta caacgagacc aaacaggtga
E  P  P  Y   I  E  A   H  H  R   V  C  T  Y   N  E  T   K  Q  V

ctgtcaagct gcccaactgt gccccgggag tcgacccctt ctacacctat cccgtggcca
T  V  K  L   P  N  C   A  P  G   V  D  P  F   Y  T  Y   P  V  A

tccgctgtga ctgcggagcc tgctccactg ccaccacgga gtgtgagacc atctgaggcc
I  R  C  D   C  G  A   C  S  T   A  T  T  E   C  E  T   I STOP

gctagctgct ctctgcagac ccacctgtgt gagcagcaca tgcagttata cttcctggat
gcaagactgt ttaatttcga ccacacccat ggaggaggtt acctgtcgcc ccttaggtcc
agctcaggca aaaggcccaa atgcagccta cttatgctaa aagttcaaaa caatattcgt
gccttcacca aaataatttc tccagctcac atacctgcaa attaattttt ctttgccttg
agtcttggaa cataatttgt gtatcacaat cctcccccaa tttggactta taatatgcta
atgatttaaa cacatgggat gtaattagga tatggggctg gaaagtcttt aaattctcat
gttctattta acctctgatc tccaaccgga tttatgatta aagggctaga aatgaacaaa
acccatgtac tagtcttcct taccccagag gaattccagc tgcaagcttc tttagggaaa
atgctccctt ccccttttaa ctgagcaatt atctacacaa gaaataagac tgctcagata
tacaaagaga gtagcttcaa tgaaaagatg tttggatttg gataattctt ttccctagca
```

FIG 4

```
aaattcgcta gctcccttaa gagtcttaat aaagaggcta cgttgggatt aaaagaaaaa
aaaacagaaa taaaatatgt aactaatagc tatctcattt agccttaaaa acttattaaa
        ^ poly(A) ?

ctaaactcat gttttagagt atgatgttct cccaaagcta tggcaaaatg gccaatcaca
agtattcttc cccatttatc atattttcaa tttaagttgt aacttactaa actcagaaat
tttatatgcg tttaggggta aaactgcatg gctggctcag aggaaaaagc ctgtgatttt
ctagctcctg cctctctaaa atcttacagt agctaattct gtggctggaa aaaacctcca
aaactctaat gttatgcaaa tgtctttaat tctggcattt ttggggttga atttaacctt
gttccttttt cataatgtgc caagaaaacc tatattaatg ccaataaagc atgtcctctg
                                              ^ poly(A) ?

tcttttggat tcatgacaac attcaagaaa gtctttttaa ttcttagtat acttggagta
```
(SEQ ID NO:78)

FIG 4

```
hLHbeta         ------MEMLQGLLLLLLLSMGGAWASREPLRPWCHPINAILAVEKEGCPVCITVNTTIC
hCGbeta         ------MEMFQGLLLLLLLSMGGTWASKEPLRPRCRPINATLAVEKEGCPVCITVNTTIC
hFSHbeta        ---------MKTLQFFFLFCCWKAICCN-S----CELTNITIAIEKEECRFCISINTTWC
hTSHbeta        ------MTALFLMSMLFGLACGQAMSF-------CIPTEYTMHIERRECAYCLTINTTIC
beta5           MKLAFLLLGPMALLLLAGYGCLGASSGNLRTFVGCAVREFTFLAKKPGCR-GLRITTDAC
                             : ::       : .        *   :  :  ::  *   : :.*  *

hLHbeta         AGYCPTMMRVLQAVLPPLP--QVVCTYRDVRFESIRLPGCPRGVDPVVSFPVALSCRCGP
hCGbeta         AGYCPTMTRVLQGVLPALP--QVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCAL
hFSHbeta        AGYCYTRDLVYKD--PARPKIQKTCTFKELVYETVRVPGCAHHADSLYTYPVATQCHCGK
hTSHbeta        AGYCMTRDINGKLFLPKYALSQDVCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGK
beta5           WGRCETWEKPILEP-PYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGA
                 * * *          *     : .*.:.:    ::.:*.*.  . .  ::.**  * *.

hLHbeta         CRRSTSDCGGPKDHPLTCDHP-------------------QLSG-----LLFL (SEQ ID NO: 6)
hCGbeta         CRRSTTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ (SEQ ID NO: 8)
hFSHbeta        CDSDSTDCTVRGLGPSYCSFG-------------------EMKE--------- (SEQ ID NO: 7)
hTSHbeta        CNTDYSDCIHEAIKTNYCTKP-------------------QKSYLVGFSV--- (SEQ ID NO: 9)
beta5           CSTATTECETI------------------------------------------ (SEQ ID NO: 2)
                *     ::*
```

FIG. 5

	beta5	hFSH	hCG	hLH	hTSH
beta5	--	36 %	31 %	35 %	34 %
hFSH	50 %	--	40 %	41 %	40 %
hCG	48 %	60 %	--	86 %	47 %
hLH	56 %	60 %	90 %	--	41 %
hTSH	50 %	58 %	59 %	53 %	--

FIG. 6

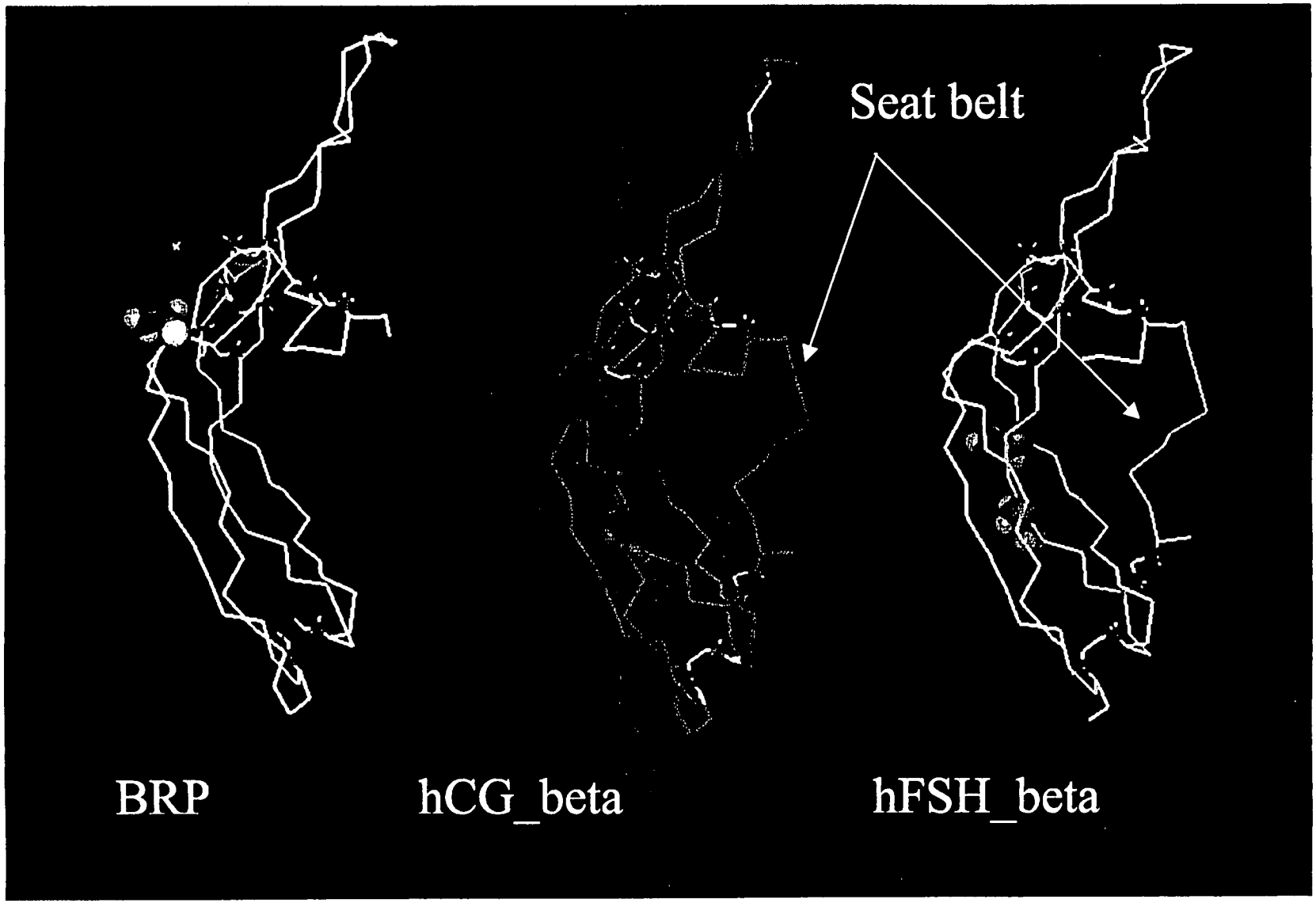


FIG. 7A

N-carbohydrate sites

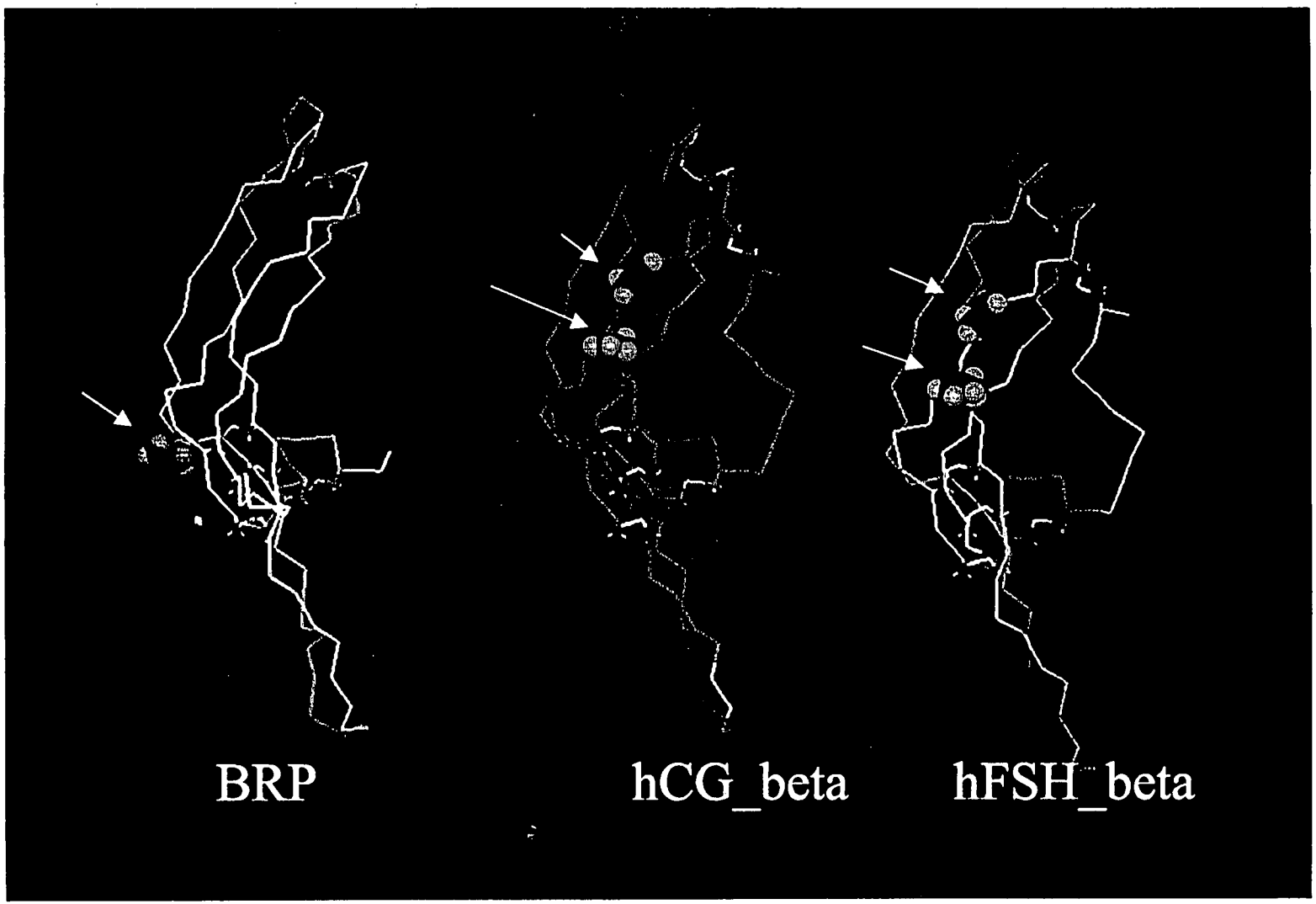


FIG. 7B

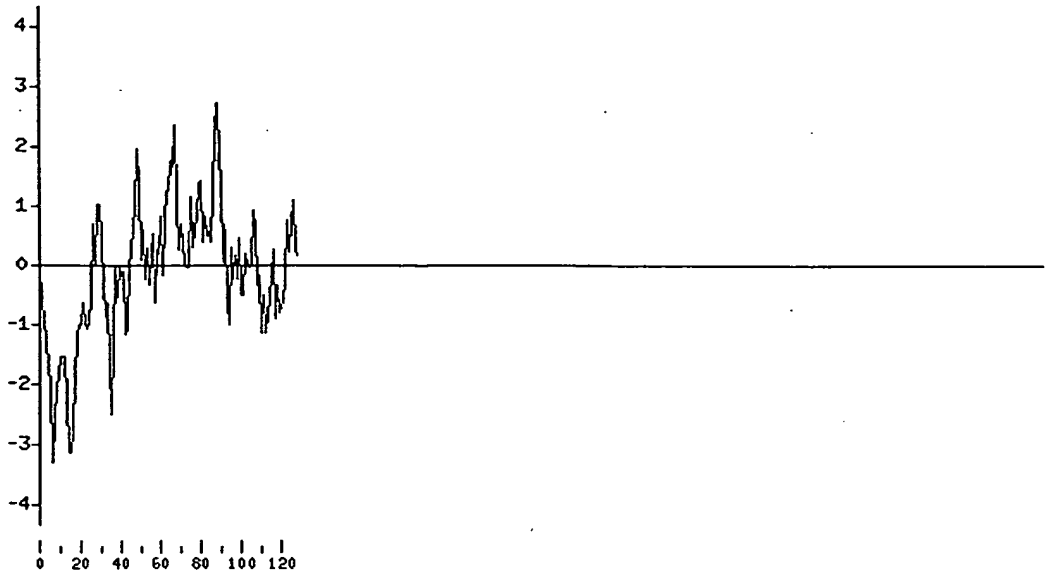


FIG. 8

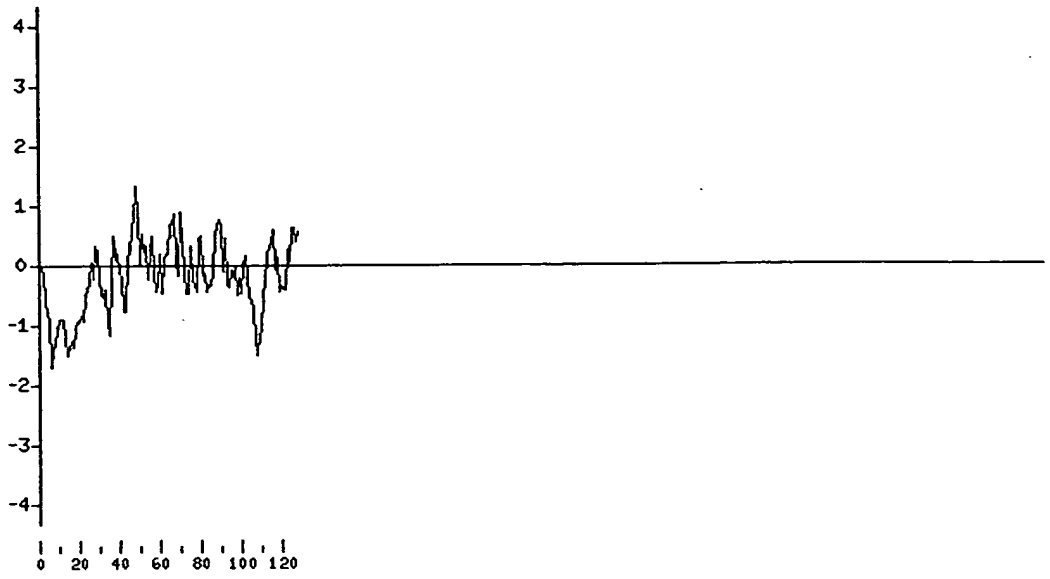


FIG. 9

MEMFQGLLLLLLLSMGGTWASKEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYC
ETWEKPILEPPYIEAHHRVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRR
STTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSPSRLPGPSDTPILPQ (SEQ ID
NO:13)

FIG. 10

MKLAFLLLGPMALLLLAGYGCLGASSGNLRTFVGCAVREFTFLAKKPGCRGLRITTDA
CWGRCETWEKPILEPPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDC
GACSTATTEC**TVRGLGPSYCSFGEMKE** (SEQ ID NO: 14)

FIG. 11

```
mouse     ------------------------------------------------------------
rat       GGGGGAGGGAGGGGCCGAAGTGGCCAGGGTTGGTATGATCCCCAGCCATGAGAGACATCC
human     ------------------------------------------------------------

mouse     ------------------------------------------------------------
rat       CAGGGGACAGTGCATAGAAGGATGGCATACACACAAGTGGCTGCTCATTGCCTTCCAGAG
human     ------------------------------------------------------------

mouse     ------------------------------------------------------------
rat       TAGCTGAGGCAAGGAAGCAAGCACCCCACACATTCCCACCCAAGGCAGAGAGGATCAACA
human     ------------------------------------------------------------

mouse     ------------------------------------------------------------CG
rat       GTGCCACCCAGGCACACCTCACAGTCGGAAGACCCAGAAGCCTGGCTTGCTGGGGGAGAG
human     ----------------------------------CGGCACGAGGCAGCAGGAGGCACA

mouse     GCACG-TAGGGGAGTCTTCAGTTGCTGTTGGACTGTCCTTTGCAGATGCCCATGGCA---
rat       ACACAACTGCAAAGACTTCCCTTCCCACC---CACTCCTTTTCAGATGCCCATGGCA---
human     GGAAAACTGCAAGCCGCTCTGTTCCTGGG---C--CTCGGAAGTGATGCCTATGGCGTCC
            *     *         **  ** *       *    *      ****** *****

mouse     CCACGAGTCTTGCTCCTTTGCCTGCTGGGCCTGGCAGTCACTGAAGGGCATAGCCCAGAG
rat       CCTCGAGTCTTGCTCTTCTGCCTGCTGGGTCTGGCAGTCACTGAAGGGCATGGCCTGGAG
human     CCTCAAACCCTGGTCCTCTATCTGCTGGTCCTGGCAGTCACTGAAGCCTGGGGCCAGGAG
          ** * *  * ** ** * *  *******  ****************      ***  ***

mouse     ACAGCC------ATCCCAGGCTGCCACTTGCACCCCTTCAATGTGACGGTGCGCAGTGAT
rat       GCAGCCGTCCCAATCCCAGGCTGCCACTTGCACCCCTTTAACGTGACAGTGCGAAGTGAT
human     GCAGTC------ATCCCAGGCTGCCACTTGCACCCCTTCAATGTGACAGTGCGAAGTGAC
           *** *       *************************** ** ***** ***** *****

mouse     CGCCTCGGCACTTGCCAGGGCTCCCACGTGGCACAGGCCTGTGTAGGACACTGTGAGTCT
rat       CGCCATGGCACCTGCCAGGGCTCCCATGTGGCACAGGCGTGTGTAGGACACTGTGAGTCT
human     CGCCAAGGCACCTGCCAGGGCTCCCACGTGGCACAGGCCTGTGTGGGCCACTGTGAGTCC
          ****  ***** ************** *********** ***** ** ***********

mouse     AGTGCTTTCCCTTCCCGGTACTCTGTGCTGGTGGCCAGTGGCTATCGGCACAACATCACC
rat       AGTGCTTTCCCTTCTCGGTACTCTGTGCTGGTTGCCAGTGGCTATCGACACAACATCACC
human     AGCGCCTTCCCTTCTCGGTACTCTGTGCTGGTGGCCAGTGGTTACCGACACAACATCACC
          ** ** ******** ***************** ******** ** ** ************

mouse     TCTTCCTCCCAGTGCTGCACCATCAGCAGCCTCAGAAAGGTGAGGGTGTGGCTGCAGTGC
rat       TCTGTCTCTCAGTGCTGTACCATCAGCAGCCTTAAAAAGGTGAGGGTGTGGCTGCACTGC
human     TCCGTCTCTCAGTGCTGCACCATCAGTGGCCTGAAGAAGGTCAAAGTACAGCTGCAGTGT
          **   *** ******** ********  **** *  ***** *  **   ****** **

mouse     GTGGGGAACCAGCGTGGGGAGCTTGAGATCTTTACTGCAAGGGCCTGCCAGTGTGATATG
rat       GTGGGGAACCAGCGTGGGGAGCTCGAGATCTTCACGGCTAGGGCCTGCCAGTGTGATATG
human     GTGGGGAGCCGGAGGGAGGAGCTCGAGATCTTAACGGCCAGGGCCTGCCAGTGTGACATG
          ******* ** * * * ****** ******** ** ** ****************** ***

mouse     TGCCGTTTCTCCCGCTACTAGTCC-CCGAAGCTCAGGC-TCCGGTCCTGCCACTGACATG
rat       TGCCGTCTCTCCCGCTACTAGGCC-CCGAAGCTCAGGCCTCCAGTCCTGCCACTGATAGG
human     TGTCGCCTCTCTCGCTACTAGCCCATCCTCTCCCCTCCTTCCTCCCCTGGGTCACAGGGC
          ** **  **** ********* **  *    * *   * ***   ****   *  *

mouse     TCATGGGTATCTCAAACTCGGGGC-TCT---GACCCTCTTTATCG---TCTGTGAAGATG
rat       TCGTGCTTCTCTCAGAC-CAGCCC-TCTTTGGAGTCTGAAGATGGGGCTTCGCCTCTGTT
human     TTGACATTCTGGTGGGGGAAACCTGTGTTCAAGATTCAAAAACTGGAAGGAGCTCCAGCC
          *      * *                 * *              *  *      *

mouse     AGGTTGG---CCCTCTCAGCAGTCTCCTT------------GCTACATTCTCCTTCGCTC
rat       TACCTGG---CCTCCTCAGCAGTCTCACT------------GCTGCTTTCTCCTTCACCC
human     CTGATGGTTACTTGCTATGGAATTTTTTTAAATAAGGGGAGGGTTGTTCCAGCTTTGATC
              ***   *   **  * * * *  *             * *   * *  ***    *

mouse     CTGTCCTCAATAAAGCAAGCAATGCTTG--------------------------------
rat       CTGTCCTCAATAAAGCAGGCAGTGCTTG--------------------------------
human     CTTTGTAAGATTTTGTGACTGTCACCTGAGAAGAGGGGAGTTTCTGCTTCTTCCCTGCCT
          ** *      **   *          * **

mouse     ------------------------------------------------------------
```

FIG 12

```
rat             ------------------------------------------------------------
human           CTGCCTGGCCCTTCTAAACCAATCTTTCATCATTTTACTTCCCTCTTTGCCCTTACCCCT

mouse           ----------------------  (SEQ ID NO:19)
rat             ----------------------  (SEQ ID NO:21)
human           AAATAAAGCAAGCAGTTCTTG   (SEQ ID NO:17)
```


FIG 12

```
mouse       MPMA-PRVLLLCLLGLAVTEGHSPETA--IPGCHLHPFNVTVRSDRLGTCQGSHVAQACV
rat         MPMA-PRVLLFCLLGLAVTEGHGLEAAVPIPGCHLHPFNVTVRSDRHGTCQGSHVAQACV
human       MPMASPQTLVLYLLVLAVTEAWGQEAV--IPGCHLHPFNVTVRSDRQGTCQGSHVAQACV
            **** *:.*:: ** *****. . *:.  ****************** ************
                                     ^

mouse       GHCESSAFPSRYSVLVASGYRHNITSSSQCCTISSLRKVRVWLQCVGNQRGELEIFTARA
rat         GHCESSAFPSRYSVLVASGYRHNITSVSQCCTISSLKKVRVWLHCVGNQRGELEIFTARA
human       GHCESSAFPSRYSVLVASGYRHNITSVSQCCTISGLKKVKVQLQCVGSRREELEILTARA
            **************************** *******.*:**:* *:****.::* ****:****

mouse       CQCDMCRFSRY  Seq. ID No: 20
rat         CQCDMCRLSRY  Seq. ID No: 22
human       CQCDMCRLSRY  Seq. ID No: 18
            *******.***
```

FIG 13

```
...1 AGATGGCGAAGAAAATTCCAGGGAAGGGAGAATCACTGCACAGAGGGCTG
..51 ACACACAGGTCCTTTCCAGAGACAGCTGCTCACACTCACACCCATACACA
.101 CACACACACACACACAAAGGCAGATACAGGGAAAAGGCAGCACCATTCAG
.151 GCACACCTCACCTGTCAGACCAGCCAGCCCTGGCTCACTCACCTGGAATG
.201 CAGTATTTAAAGAACTCGCCATCCCACCTGCACACCCACGTAGAGACATC
.251 TCCCCACTGTGTTTCAGATGCCTATGGCGTCCCCTCAAACCCTGGTCCTC
 301 TATCTGCTGGTCCTGGCAGTCACTGAAGCCTGGGGCCAGGAGGCAGTCAT
.351 CCCAGGCTGCCACTTGCACCGTGAGTACCTCTGGGACCGGAGGGCTAGGA
.401 GCAGTGGAGGTTCTGGGTGGGAGCAAAGAGCTGACAGAGTGGACGGTGGG
 451 GCAGGCAGCACCCTAAAGGGCCCCACACTGAGGCACAGGCAACGGGAGCT
.501 GGGGCGAGGCAAACCTTGGCAGAGGCGCCGTCTACTGCTTGCCTATCTCC
.551 TTCTAGCCTTCAATGTGACAGTGCGAAGTGACCGCCAAGGCACCTGCCAG
.601 GGCTCCCACGTGGCACAGGCCTGTGTGGGCCACTGTGAGTCCAGCGCCTT
 651 CCCTTCTCGGTACTCTGTGCTGGTGGCCAGTGGTTACCGACACAACATCA
.701 CCTCCGTCTCTCAGTGCTGCACCATCAGTGGCCTGAAGAAGGTGAGGAGG
.751 GCCCGGGCCCGGTGGATGGACGCTGGGGTCGCGGGAAGACCAGAGAGATG
.801 GAGATCCTAGACAGCCCTGAGAAAGGGGACTGCAGCACGGACTCCCCTCT
.851 CCCGCAGGTCAAAGTACAGCTGCAGTGTGTGGGGAGCCGGAGGGAGGAGC
.901 TCGAGATCTTCACGGCCAGGGCCTGCCAGTGTGACATGTGTCGCCTCTCT
.951 CGCTACTAGCCCATCCTCTCCCCTCCTTCCTCCCCTGGGTCACAGGGCTT
1001 GACATTCTGGTGGGGGAAACCTGTGTTCAAGATTCAAAAACTGGAAGGAG
1051 CTCCAGCCCTGATGGTTACTTGCTATGGAATTTTTTTAAATAAGGGGAGG
1101 GTTGTTCCAGCTTTGATCCTTTGTAAGATTTTGTGACTGTCACCTGAGAA
1151 GAGGGGAGTTTCTGCTTCTTCCCTGCCTCTGCCTGGCCCTTCTAAACCAA
1201 TCTTTCATCATTTTACTTCCCTCT(SEQ ID NO:23)
```

FIG. 14

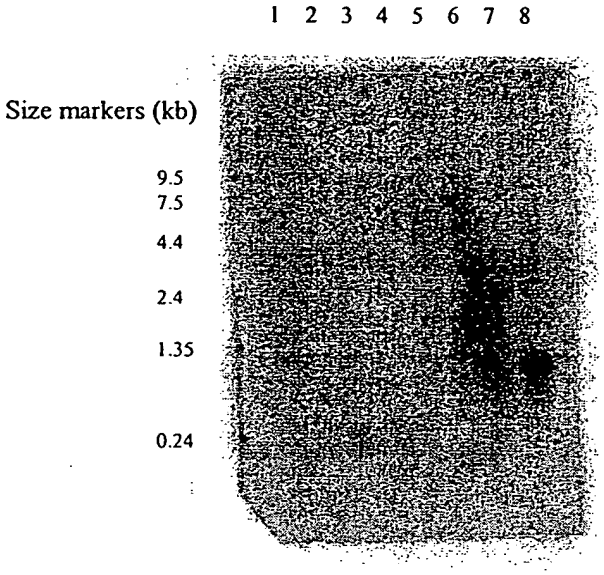
```
hFSHa   MDYYRKYAAIFLVTLSVFLHVLHSAPDVQDCPECTLQENPFFS-------QPG
hARP       MPMASPQTLVLYLLVLAVTEAWGQEAVIPGCHLHPFNVTVRSDRQGTCQG
hFSHb        MKTLQFFFLFCCWKAICC--------NSCELTNITIAIEKEECRFCIS

hFSHa      APILQ-CMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVM
hARP       SHVAQACVGHCESSAFPSRYSVLVASGYRHNITSVSQCCTISGLKKVKVQ
hFSHb      INTTW-CAGYCYTRDLVYKD---------PARPKIQKTCTFKELVYETVR

hFSHa      ---------GGFKVENHTACHCSTCYYHKS (SEQ ID NO: 10)
hARP       -LQCVGSRREELEIFTARACQCDMCRLSRY (SEQ ID NO: 2)
hFSHb      VPGCAHHADSLYTYPVATQCHCGKCDSDSTDCTVRGLGPSYCSFGEMKE (SEQ ID NO: 11)
```

FIG. 15

```
DNA: AGATGGCGAAGAAAATTCCAGGGAAGGGAGAATCACTGCACAGAGGGCTGA
DNA: CACACAGGTCCTTTCCAGAGACAGCTGCTCACACTCACACCCATACACACA
DNA: CACACACACACACAAAGGCAGATACAGGGAAAAGGCAGCACCATTCAGGCA
DNA: CACCTCACCTGTCAGACCAGCCAGCCCTGGCTCACTCACCTGGAATGCAGT
DNA: ATTTAAAGAACTCGCCATCCCACCTGCACACCCACGTAGAGACATCTCCCC
DNA: ACTGTGTTTCAGATGCCTATGGCGTCCCCTCAAACCCTGGTCCTCTATCTG
 +1:              M  P  M  A  S  P  Q  T  L  V  L  Y  L

DNA: CTGGTCCTGGCAGTCACTGAAGCCTGGGGCCAGGAGGCAGTCATCCCAGGC
 +1: L  V  L  A  V  T  E  A  W  G  Q  E  A  V  I  P  G

DNA: TGCCACTTGCACCGTGAGTACCTCTGGGACCGGAGGGCTAGGAGCAGTGGA
 +1: C  H  L  H  P

DNA: GGTTCTGGGTGGGAGCAAAGAGCTGACAGAGTGGACGGTGGGGCAGGCAGC
DNA: ACCCTAAAGGGCCCCACACTGAGGCACAGGCAACGGGAGCTGGGGCGAGGC
DNA: AAACCTTGGCAGAGGCGCCGTCTACTGCTTGCCTATCTCCTTCTAGCCTTC
 +1:                                                    F

DNA: AATGTGACAGTGCGAAGTGACCGCCAAGGCACCTGCCAGGGCTCCCACGTG
 +1: N  V  T  V  R  S  D  R  Q  G  T  C  Q  G  S  H  V

DNA: GCACAGGCCTGTGTGGGCCACTGTGAGTCCAGCGCCTTCCCTTCTCGGTAC
 +1: A  Q  A  C  V  G  H  C  E  S  S  A  F  P  S  R  Y

DNA: TCTGTGCTGGTGGCCAGTGGTTACCGACACAACATCACCTCCGTCTCTCAG
 +1: S  V  L  V  A  S  G  Y  R  H  N  I  T  S  V  S  Q

DNA: TGCTGCACCATCAGTGGCCTGAAGAAGGTGAGGAGGGCCCGGGCCCGGTGG
 +1: C  C  T  I  S  G  L  K  K

DNA: ATGGACGCTGGGGTCGCGGGAAGACCAGAGAGATGGAGATCCTAGACAGCC
DNA: CTGAGAAAGGGGACTGCAGCACGGACTCCCCTCTCCCGCAGGTCAAAGTAC
 +3:                                                V  K  V  Q

DNA: AGCTGCAGTGTGTGGGGAGCCGGAGGGAGGAGCTCGAGATCTTCACGGCCA
 +3:    L  Q  C  V  G  S  R  R  E  E  L  E  I  F  T  A  R

DNA: GGGCCTGCCAGTGTGACATGTGTCGCCTCTCTCGCTACTAGCCCATCCTCT
 +3:    A  C  Q  C  D  M  C  R  L  S  R  Y  *

DNA: CCCCTCCTTCCTCCCCTGGGTCACAGGGCTTGACATTCTGGTGGGGGAAAC
DNA: CTGTGTTCAAGATTCAAAAACTGGAAGGAGCTCCAGCCCTGATGGTTACTT
DNA: GCTATGGAATTTTTTTAAATAAGGGGAGGGTTGTTCCAGCTTTGATCCTTT
DNA: GTAAGATTTTGTGACTGTCACCTGAGAAGAGGGGAGTTTCTGCTTCTTCCC
DNA: TGCCTCTGCCTGGCCCTTCTAAACCAATCTTTCATCATTTTACTTCCCTCT (SEQ ID NO:79)
```

FIG. 16

Northern Blot of ARP - human cDNA probe and blot
(C. He – 3/24/00: 4 day exposure)



Lanes:
1 – heart
2 – brain
3 – placenta
4 – lung
5 – liver
6 – skeletal muscle
7 – kidney
8 – pancreas

FIG. 17

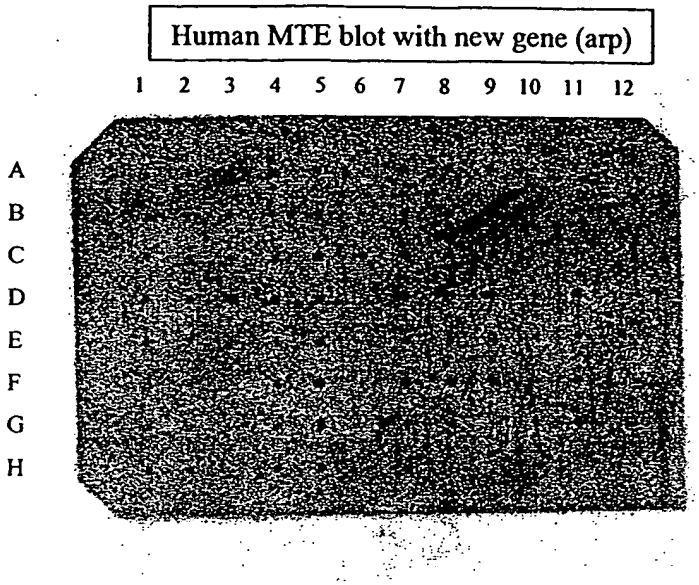
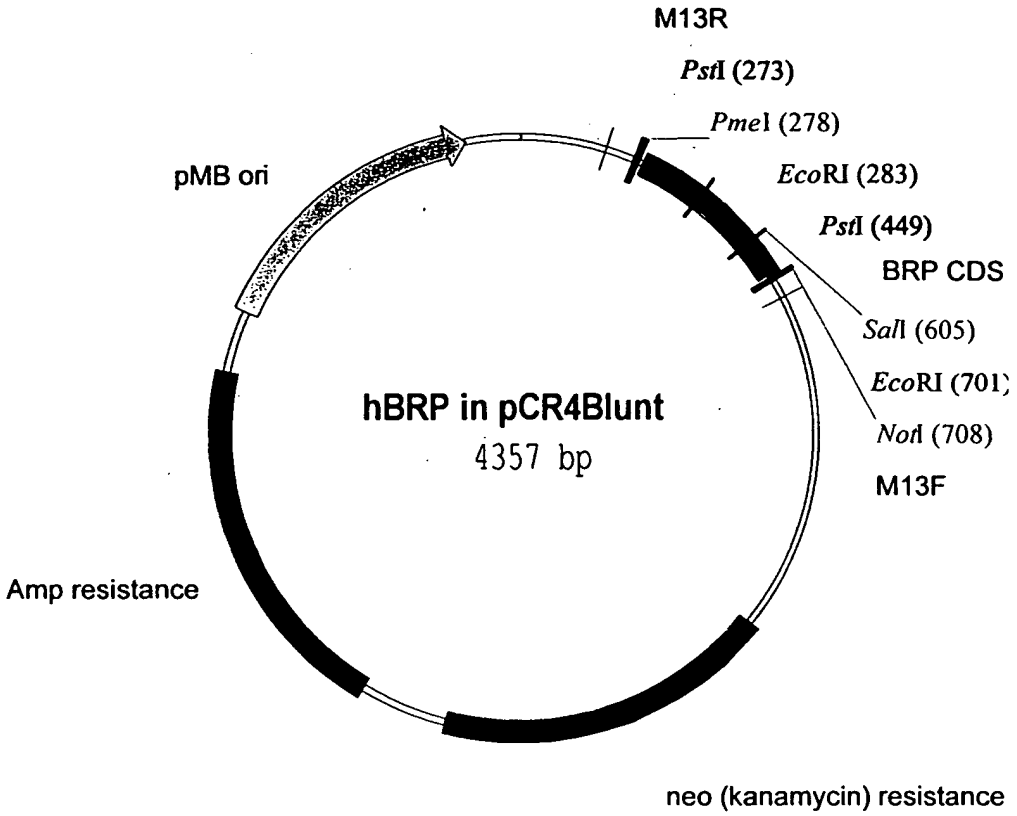

Human MTE blot with new gene (arp)
1 2 3 4 5 6 7 8 9 10 11 12
A
B
C
D
E
F
G
H
pancreas = B-9
pituitary = D-3
spots near B-7 (skeletal muscle) and D-8 (uterus) appear to be non-specific /background as they are off-set from the blot spot. Ovary and testis are G-8 and F-8 respectively

FIG. 18

A.

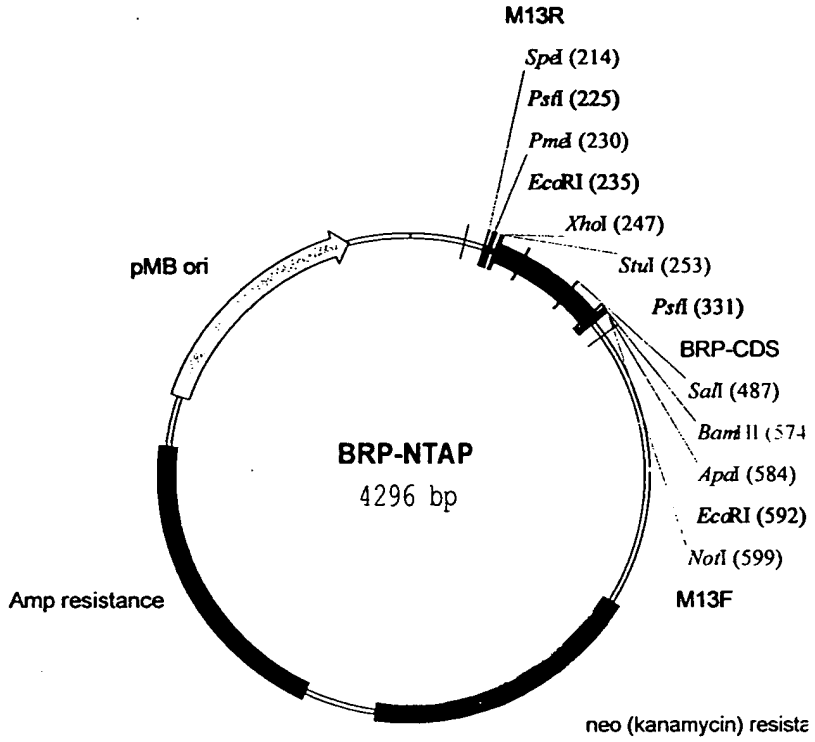


B.

```
      EcoRI
      ------
                        M  K  L  A  F  L  F  L  G  P  M  A  L  L  L  L  A  G  .
      CGAATTCGCC CTTCAGCATG AAGCTGGCAT TCCTCTTCCT TGGCCCCATG GCCCTCCTCC TTCTGGCTGG

      .  Y  G  C  V  L  G  A  S  S  G  N  L  R  T  F  V  G  C  A  V  R  E  F
      CTATGGCTGT GTCCTCGGTG CCTCCAGTGG GAACCTGCGC ACCTTTGTGG GCTGTGCCGT GAGGGAGTTT
                              PstI
                              -------
       T  F  L  A  K  K  P  G  C  R  G  L  R  I  T  T  D  A  C  W  G  R  C  E  .
      ACTTTCCTGG CCAAGAAGCC AGGCTGCAGG GGCCTTCGGA TCACCACGGA TGCCTGCTGG GGTCGCTGTG

      .. T  W  E  K  P  I  L  E  P  P  Y  I  E  A  H  H  R  V  C  T  Y  N  E  .
      AGACCTGGGA GAAACCCATT CTGGAACCCC CCTATATTGA AGCCCATCAT CGAGTCTGTA CCTACAACGA
                                                SalI
                                                -------
      .  T  K  Q  V  T  V  K  L  P  N  C  A  P  G  V  D  P  F  Y  T  Y  P  V
      GACCAAACAG GTGACTGTCA AGCTGCCCAA CTGTGCCCCG GGAGTCGACC CCTTCTACAC CTATCCCGTG
                                                                          EcoRI
       A  I  R  C  D  C  G  A  C  S  T  A  T  T  E  C  E  T  I  *  (SEQ ID NO:81)
      GCCATCCGCT GTGACTGCGG AGCCTGCTCC ACTGCCACCA CGGAGTGTGA GACCATCTGA GGCAAGGGCG (SEQ ID NO: 82)
```

FIG. 19

A.

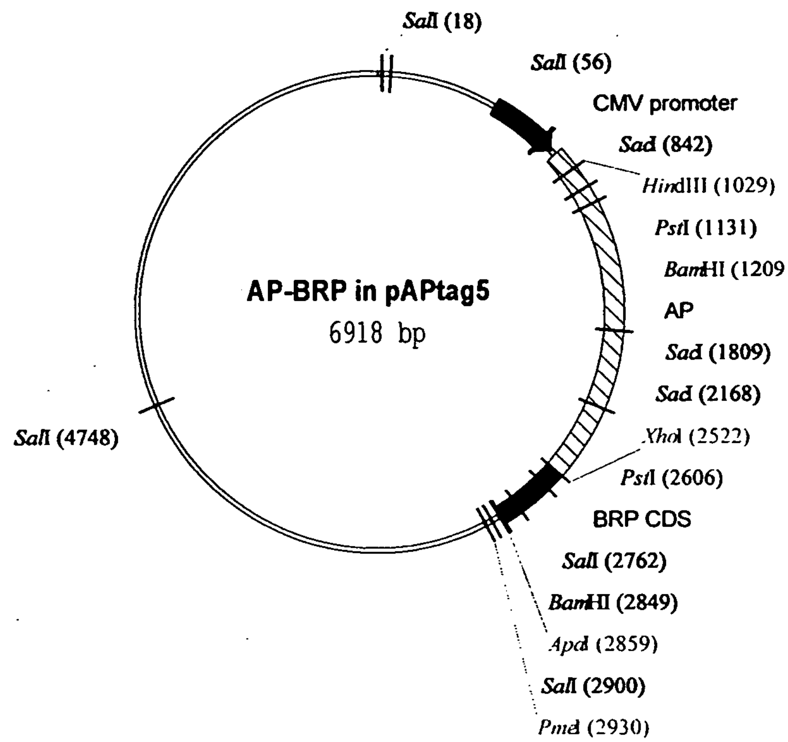


B.

```
                        PmeI
                      ~~~~~~~~~~
                PstI           EcoRI         XhoI
               ~~~~~~~         ~~~~~~~      ~~~~~~~
                                                  A  S  S  G  N  L  R  T  F  V
    1   GGACTAGTCC TGCAGGTTTA AACGAATTCG CCCTTCTCGA GGCCTCCAGT GGGAACCTGC GCACCTTTGT
                                                       PstI
                                                     ~~~~~~~
        .  G  C  A  V  R  E  F  T  F  L  A  K  K  P  G  C  R  G  L  R  I  T  T
   91   GGGCTGTGCC GTGAGGGAGT TTACTTTCCT GGCCAAGAAG CCAGGCTGCA GGGGCCTTCG GATCACCACG

         D  A  C  W  G  R  C  E  T  W  E  K  P  I  L  E  P  P  Y  I  E  A  H  H
  181   GATGCCTGCT GGGGTCGCTG TGAGACCTGG GAGAAACCCA TTCTGGAACC CCCCTATATT GAAGCCCATC
                                                                          SalI
        .. R  V  C  T  Y  N  E  T  K  Q  V  T  V  K  L  P  N  C  A  P  G  V  D
  271   ATCGAGTCTG TACCTACAAC GAGACCAAAC AGGTGACTGT CAAGCTGCCC AACTGTGCCC CGGGAGTCGA
        .
        ~
        .  P  F  Y  T  Y  P  V  A  I  R  C  D  C  G  A  C  S  T  A  T  T  E  C
  361   CCCCTTCTAC ACCTATCCCG TGGCCATCCG CTGTGACTGC GGAGCCTGCT CCACTGCCAC CACGGAGTGT
                           ApaI                  NotI
                         ~~~~~~~               ~~~~~~~~~~
                    BamHI                EcoRI
                   ~~~~~~               ~~~~~~
         E  T  I  *  (SEQ ID NO: 83)
  451   GAGACCATCT GAGGATCCGG GCCCAAGGGC GAATTCGCGG CCGCTAAATT CAATTCGCCC TATAGTGAGT
(SEQ ID NO:84)
```

FIG. 20

A.



B.

```
                                                                  Alkaline phosphatase
                                                                      <-----------
      . L  E  P  Y  T  A  C  D  L  A  P  P  A  G  T  T  D  A  A  H  P  G  Y
2451  CCTGGAGCCC TACACCGCCT GCGACCTGGC GCCCCCCGCC GGCACCACCG ACGCCGCGCA CCCGGGTTAT
      XhoI
      ~~~~~~  BRP -->
      L  E  A  S  S  G  N  L  R  T  F  V  G  C  A  V  R  E  F  T  F  L  A  K·
2521  CTCGAGGCCT CCAGTGGGAA CCTGCGCACC TTTGTGGGCT GTGCCGTGAG GGAGTTTACT TTCCTGGCCA
                PstI
                ~~~~~~
      .. K  P  G  C  R  G  L  R  I  T  T  D  A  C  W  G  R  C  E  T  W  E  K·
2591  AGAAGCCAGG CTGCAGGGGC CTTCGGATCA CCACGGATGC CTGCTGGGGT CGCTGTGAGA CCTGGGAGAA

      . P  I  L  E  P  P  Y  I  E  A  H  H  R  V  C  T  Y  N  E  T  K  Q  V
2661  ACCCATTCTG GAACCCCCCT ATATTGAAGC CCATCATCGA GTCTGTACCT ACAACGAGAC CAAACAGGTG
                                       SalI
                                       ~~~~~~
      T  V  K  L  P  N  C  A  P  G  V  D  P  F  Y  T  Y  P  V  A  I  R  C  D·
2731  ACTGTCAAGC TGCCCAACTG TGCCCCGGGA GTCGACCCCT TCTACACCTA TCCCGTGGCC ATCCGCTGTG
                                                                ApaI
                                                                ~~~~~~~
                                                          BamHI
                                                          ~~~~~~
      .. C  G  A  C  S  T  A  T  T  E  C  E  T  I  *  (SEQ ID NO:85)
2801  ACTGCGGAGC CTGCTCCACT GCCACCACGG AGTGTGAGAC CATCTGAGGA TCCGGGCCCG AACAAAAACT
(SEQ ID NO:86)
```

FIG. 21

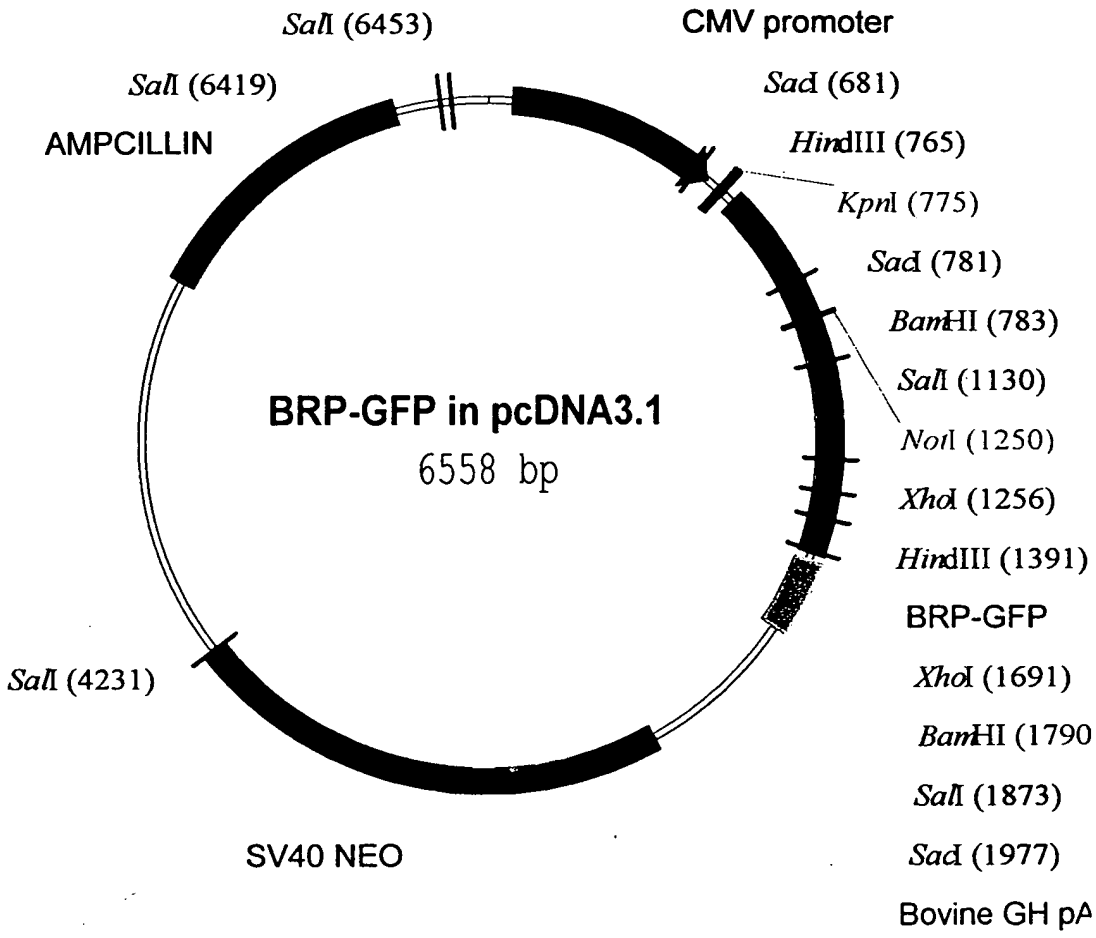

SalI (6453)
CMV promoter
SalI (6419)
SacI (681)
AMPCILLIN
HindIII (765)
KpnI (775)
SacI (781)
BamHI (783)
SalI (1130)
BRP-GFP in pcDNA3.1
6558 bp
NotI (1250)
XhoI (1256)
HindIII (1391)
BRP-GFP
SalI (4231)
XhoI (1691)
BamHI (1790
SalI (1873)
SacI (1977)
SV40 NEO
Bovine GH pA

FIG. 22

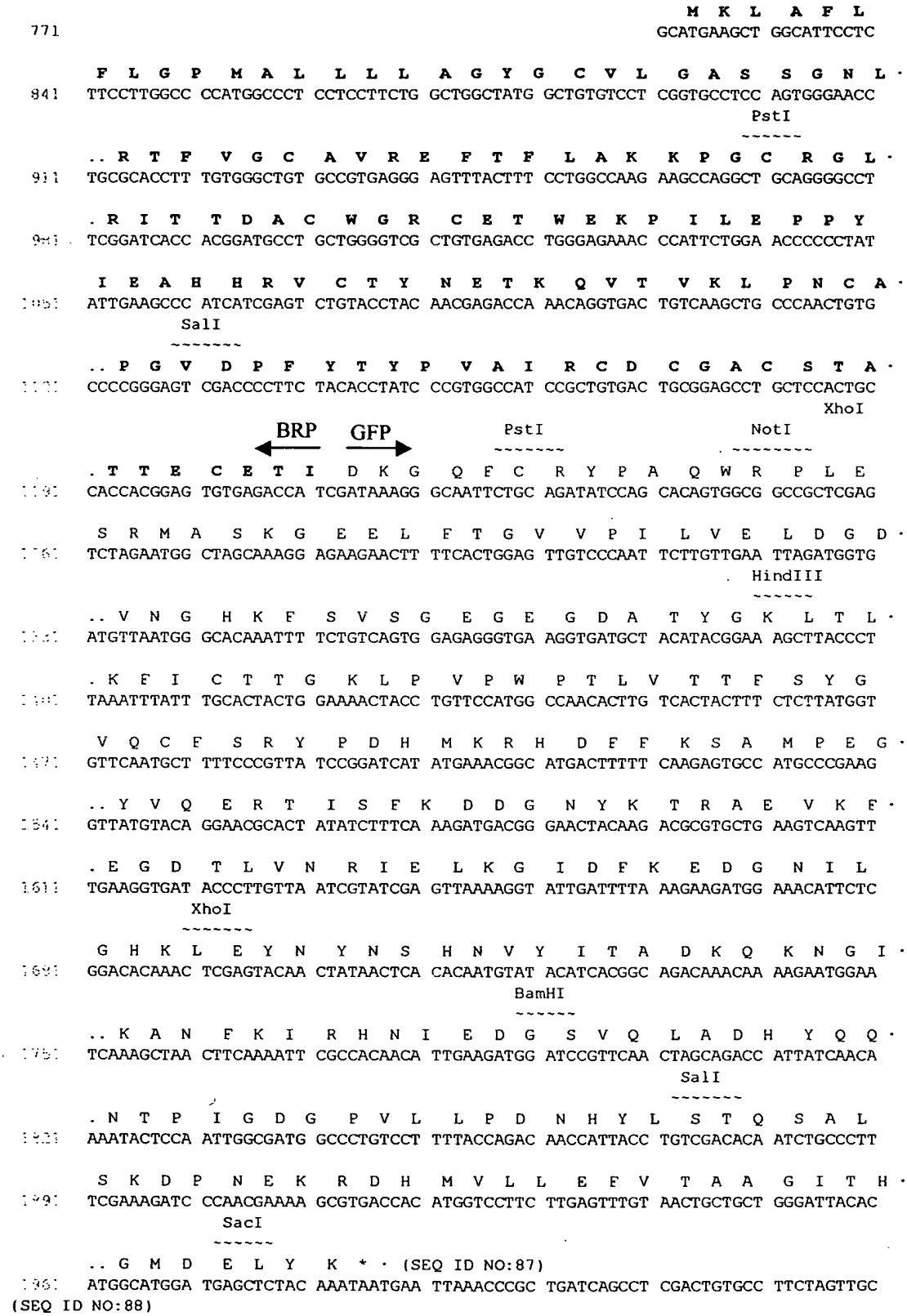
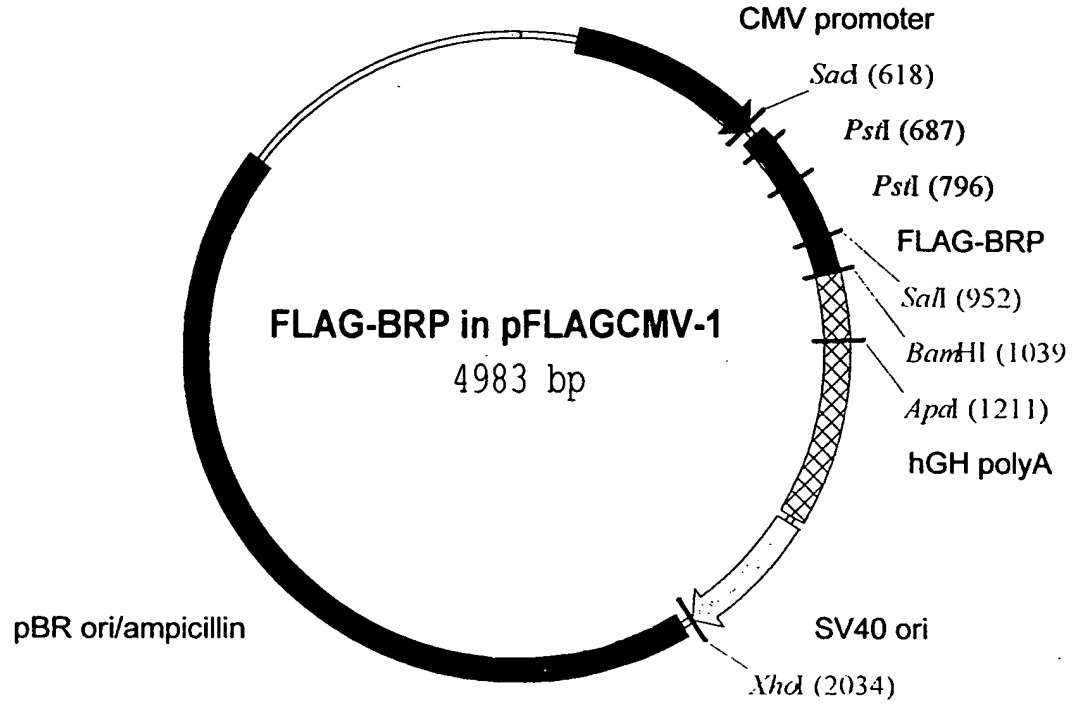

M K L A F L
771 GCATGAAGCT GGCATTCCTC
F L G P M A L L L L A G Y G C V L G A S S G N L
841 TTCCTTGGCC CCATGGCCCT CCTCCTTCTG GCTGGCTATG GCTGTGTCCT CGGTGCCTCC AGTGGGAACC
PstI
..R T F V G C A V R E F T F L A K K P G C R G L
911 TGCGCACCTT TGTGGGCTGT GCCGTGAGGG AGTTTACTTT CCTGGCCAAG AAGCCAGGCT GCAGGGGCCT
.R I T T D A C W G R C E T W E K P I L E P P Y
981 TCGGATCACC ACGGATGCCT GCTGGGGTCG CTGTGAGACC TGGGAGAAAC CCATTCTGGA ACCCCCCTAT
I E A H H R V C T Y N E T K Q V T V K L P N C A
1051 ATTGAAGCCC ATCATCGAGT CTGTACCTAC AACGAGACCA AACAGGTGAC TGTCAAGCTG CCCAACTGTG
SalI
..P G V D P F Y T Y P V A I R C D C G A C S T A
1121 CCCCGGGAGT CGACCCCTTC TACACCTATC CCGTGGCCAT CCGCTGTGAC TGCGGAGCCT GCTCCACTGC
XhoI
BRP GFP PstI NotI
.T T E C E T I D K G Q F C R Y P A Q W R P L E
1191 CACCACGGAG TGTGAGACCA TCGATAAAGG GCAATTCTGC AGATATCCAG CACAGTGGCG GCCGCTCGAG
S R M A S K G E E L F T G V V P I L V E L D G D
1261 TCTAGAATGG CTAGCAAAGG AGAAGAACTT TTCACTGGAG TTGTCCCAAT TCTTGTTGAA TTAGATGGTG
HindIII
..V N G H K F S V S G E G E G D A T Y G K L T L
1331 ATGTTAATGG GCACAAATTT TCTGTCAGTG GAGAGGGTGA AGGTGATGCT ACATACGGAA AGCTTACCCT
.K F I C T T G K L P V P W P T L V T T F S Y G
1401 TAAATTTATT TGCACTACTG GAAAACTACC TGTTCCATGG CCAACACTTG TCACTACTTT CTCTTATGGT
V Q C F S R Y P D H M K R H D F F K S A M P E G
1471 GTTCAATGCT TTTCCCGTTA TCCGGATCAT ATGAAACGGC ATGACTTTTT CAAGAGTGCC ATGCCCGAAG
..Y V Q E R T I S F K D D G N Y K T R A E V K F
1541 GTTATGTACA GGAACGCACT ATATCTTTCA AAGATGACGG GAACTACAAG ACGCGTGCTG AAGTCAAGTT
.E G D T L V N R I E L K G I D F K E D G N I L
1611 TGAAGGTGAT ACCCTTGTTA ATCGTATCGA GTTAAAAGGT ATTGATTTTA AAGAAGATGG AAACATTCTC
XhoI
G H K L E Y N Y N S H N V Y I T A D K Q K N G I
1681 GGACACAAAC TCGAGTACAA CTATAACTCA CACAATGTAT ACATCACGGC AGACAAACAA AAGAATGGAA
BamHI
..K A N F K I R H N I E D G S V Q L A D H Y Q Q
1751 TCAAAGCTAA CTTCAAAATT CGCCACAACA TTGAAGATGG ATCCGTTCAA CTAGCAGACC ATTATCAACA
SalI
.N T P I G D G P V L L P D N H Y L S T Q S A L
1821 AAATACTCCA ATTGGCGATG GCCCTGTCCT TTTACCAGAC AACCATTACC TGTCGACACA ATCTGCCCTT
S K D P N E K R D H M V L L E F V T A A G I T H
1891 TCGAAAGATC CCAACGAAAA GCGTGACCAC ATGGTCCTTC TTGAGTTTGT AACTGCTGCT GGGATTACAC
SacI
..G M D E L Y K * · (SEQ ID NO:87)
1961 ATGGCATGGA TGAGCTCTAC AAATAATGAA TTAAACCCGC TGATCAGCCT CGACTGTGCC TTCTAGTTGC
(SEQ ID NO:88)

FIG. 23

A.



B.

```
                                                                  SacI
                                                                  ~~~~~~~
581  CCGTTGACGC AAATGGGCGG TAGGCGTGTA CGGTGGGAGG TCTATATAAG CAGAGCTCGT TTAGTGAACC
                                                                  PstI
                          Mouse preprotrypsin leader              ~~~~~~~   FLAG
                                                                            ------>
                          M  S  A  L  L  I  L  A  L  V  G  A  A  V  A  D  Y  K
631  GTCAGAATTA ATTCACCATG TCTGCACTTC TGATCCTAGC TCTTGTTGGA GCTGCAGTTG CTGACTACAA
                     BRP
                     ---->
                  .  D  D  D  D  K  A  S  S  G  N  L  R  T  F  V  G  C  A  V  R  E  F  T
701  AGACGATGAC GACAAGGCCT CCAGTGGGAA CCTGCGCACC TTTGTGGGCT GTGCCGTGAG GGAGTTTACT
                              PstI
                              ~~~~~~
                  F  L  A  K  K  P  G  C  R  G  L  R  I  T  T  D  A  C  W  G  R  C  E  T
771  TTCCTGGCCA AGAAGCCAGG CTGCAGGGGC CTTCGGATCA CCACGGATGC CTGCTGGGGT CGCTGTGAGA
                  .. W  E  K  P  I  L  E  P  P  Y  I  E  A  H  H  R  V  C  T  Y  N  E  T
841  CCTGGGAGAA ACCCATTCTG GAACCCCCCT ATATTGAAGC CCATCATCGA GTCTGTACCT ACAACGAGAC
                                                    SalI
                                                    ~~~~~~~
                  .  K  Q  V  T  V  K  L  P  N  C  A  P  G  V  D  P  F  Y  T  Y  P  V  A
911  CAAACAGGTG ACTGTCAAGC TGCCCAACTG TGCCCCGGGA GTCGACCCCT TCTACACCTA TCCCGTGGCC
                                                                  BamHI
                                                                  ~~~~~~
                  I  R  C  D  C  G  A  C  S  T  A  T  T  E  C  E  T  I  *  (SEQ ID NO: 89)
981  ATCCGCTGTG ACTGCGGAGC CTGCTCCACT GCCACCACGG AGTGTGAGAC CATCTGAGGA TCCCGGGTGG
(SEQ ID NO:90)
```

FIG. 24

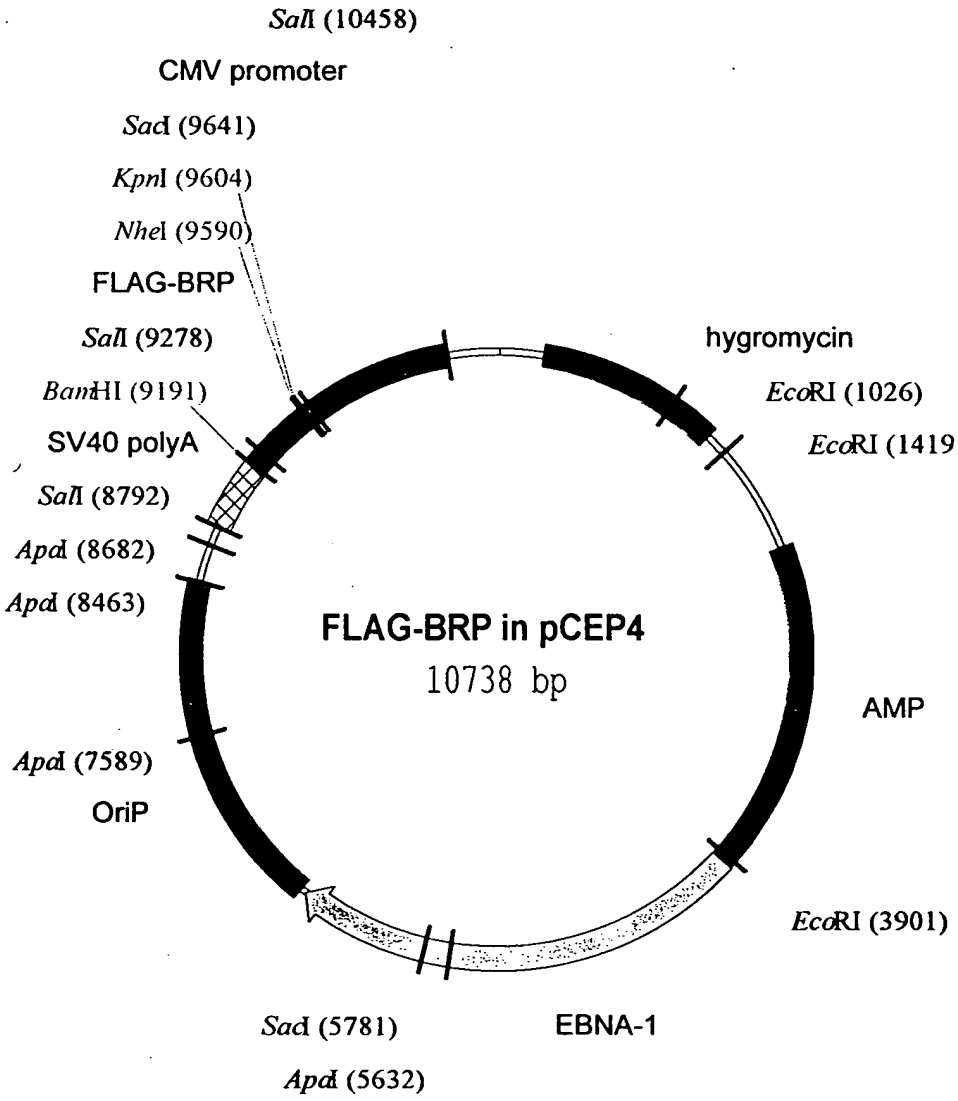
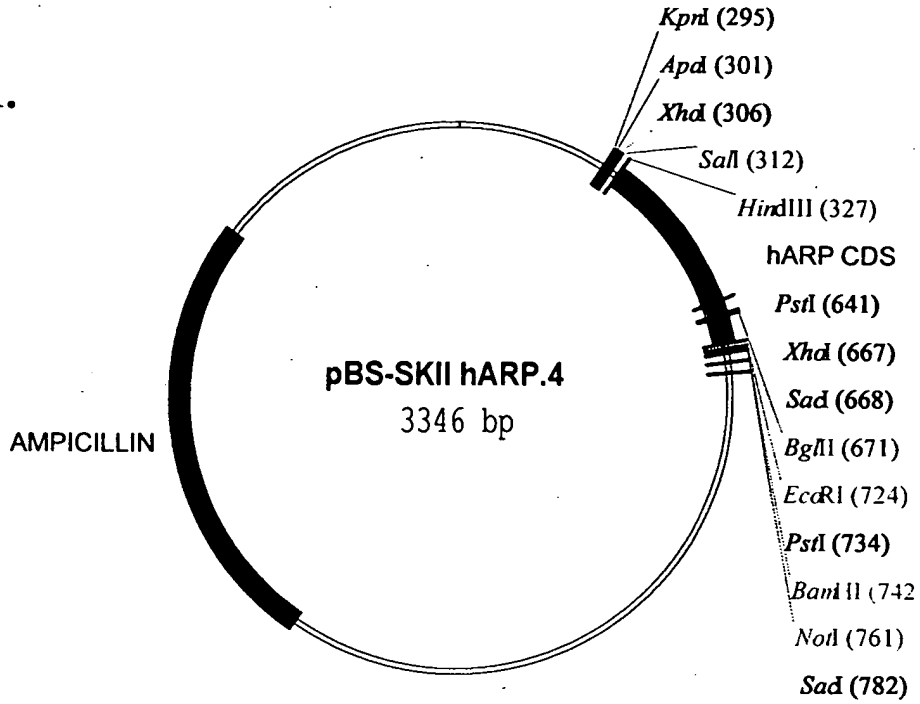

SalI (10458)
CMV promoter
SacI (9641)
KpnI (9604)
NheI (9590)
FLAG-BRP
SalI (9278)
BamHI (9191)
SV40 polyA
SalI (8792)
ApaI (8682)
ApaI (8463)
ApaI (7589)
OriP
SacI (5781)
ApaI (5632)
EBNA-1
EcoRI (3901)
AMP
EcoRI (1419
EcoRI (1026)
hygromycin
FLAG-BRP in pCEP4
10738 bp

FIG. 25

A.



B.

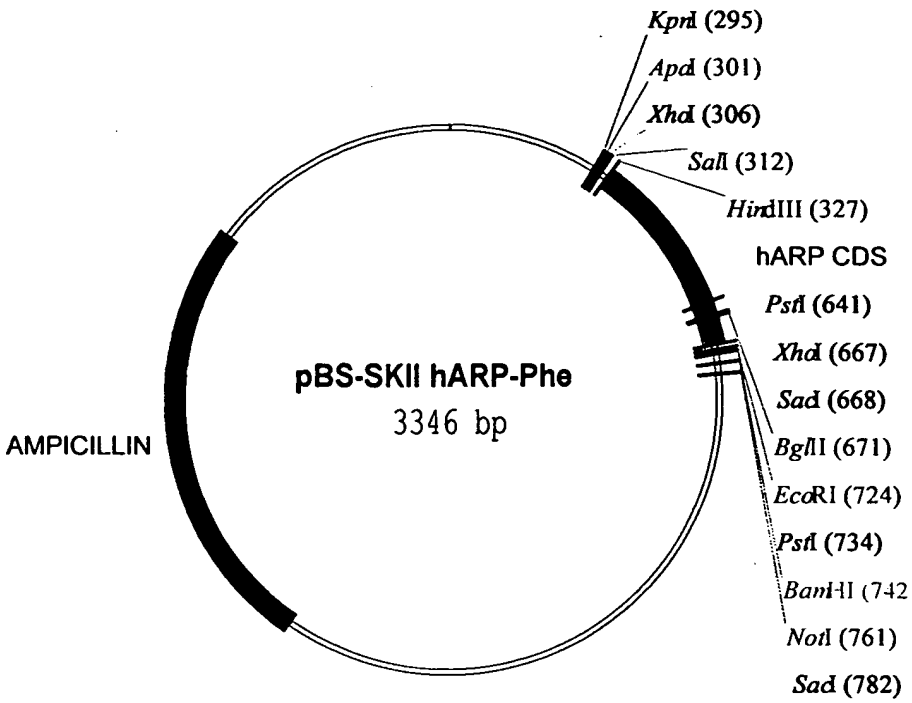
```
                    ApaI        XhoI
                    -------     -------
          KpnI                        SalI          HindIII
          -------                     ------        -------
                                                                M  P  M  A  S
281:  GGCGAATTGG GTACCGGGCC CCCCCTCGAG GTCGACGGTA TCGATAAGCT TAGTGATGCC TATGGCGTCC

       P  Q  T  L  V  L  Y  L  L  V  L  A  V  T  E  A  W  G  Q  E  A  V  I  P  .
351:  CCTCAAACCC TGGTCCTCTA TCTGCTGGTC CTGGCAGTCA CTGAAGCCTG GGGCCAGGAG GCAGTCATCC

       .  .  G  C  H  L  H  P  F  N  V  T  V  R  S  D  R  Q  G  T  C  Q  G  S  H  .
421:  CAGGCTGCCA CTTGCACCCC TTCAATGTGA CAGTGCGAAG TGACCGCCAA GGCACCTGCC AGGGCTCCCA

       .  V  A  Q  A  C  V  G  H  C  E  S  S  A  F  P  S  R  Y  S  V  L  V  A
491:  CGTGGCACAG GCCTGTGTGG GCCACTGTGA GTCCAGCGCC TTCCCTTCTC GGTACTCTGT GCTGGTGGCC

       S  G  Y  R  H  N  I  T  S  V  S  Q  C  C  T  I  S  G  L  K  K  V  K  V  .
561:  AGTGGTTACC GACACAACAT CACCTCCGTC TCTCAGTGCT GCACCATCAG TGGCCTGAAG AAGGTCAAAG
                                                  XhoI
                                                  -------
            PstI                                  SacI  BglII
            -------                               -------------
       .  .  Q  L  Q  C  V  G  S  R  R  E  E  L  E  I  L  T  A  R  A  C  Q  C  D  .
631:  TACAGCTGCA GTGTGTGGGG AGCCGGAGGG AGGAGCTCGA GATCTTAACG GCCAGGGCCT GCCAGTGTGA
                                        PstI
                                        ------
                                EcoRI                   BamHI                   NotI
                                -------                 --------                -------
       .  M  C  R  L  S  R  Y  (SEQ ID NO:91)
701:  CATGTGTCGC CTCTCTCGCT ACGAATTCCT GCAGCCCGGG GGATCCACTA GTTCTAGAGC GGCCGCCACC
(SEQ ID NO:92)
```

FIG. 26

```
    M  P  M  A  S  P  Q  T  L  V  L  Y  L  L  V  L  A  V  T  E
1   ATGCCTATGGCGTCCCCTCAAACCCTGGTCCTCTATCTGCTGGTCCTGGCAGTCACTGAA   60

    A  W  G  Q  E  A  V  I  P  G  C  H  L  H  P  F  N  V  T  V
61  GCCTGGGGCCAGGAGGCAGTCATCCCAGGCTGCCACTTGCACCCCTTCAATGTGACAGTG   120

    R  S  D  R  Q  G  T  C  Q  G  S  H  V  A  Q  A  C  V  G  H
121 CGAAGTGACCGCCAAGGCACCTGCCAGGGCTCCCACGTGGCACAGGCCTGTGTGGGCCAC   180

    C  E  S  S  A  F  P  S  R  Y  S  V  L  V  A  S  G  Y  R  H
181 TGTGAGTCCAGCGCCTTCCCTTCTCGGTACTCTGTGCTGGTGGCCAGTGGTTACCGACAC   240

    N  I  T  S  V  S  Q  C  C  T  I  S  G  L  K  K  V  K  V  Q
241 AACATCACCTCCGTCTCTCAGTGCTGCACCATCAGTGGCCTGAAGAAGGTCAAAGTACAG   300

                                                F
    L  Q  C  V  G  S  R  R  E  E  L  E  I  L  T  A  R  A  C  Q
301 CTGCAGTGTGTGGGGAGCCGGAGGGAGGAGCTCGAGATCTTAACGGCCAGGGCCTGCCAG   360
                                                C

    C  D  M  C  R  L  S  R  Y  *  (SEQ ID NO: 93)
361 TGTGACATGTGTCGCCTCTCTCGCTACTAG  390  (SEQ ID NO: 94)
```

FIG. 27

A.



B.

```
                KpnI          XhoI
                ~~~~~~~       ~~~~~~~
                      ApaI            SalI          HindIII
                      ~~~~~~~         ~~~~~~        ~~~~~~~
                                                              M  P   M  A  S
281  GGCGAATTGG GTACCGGGCC CCCCCTCGAG GTCGACGGTA TCGATAAGCT TAGTGATGCC TATGGCGTCC

      P  Q  T  L  V  L  Y   L  L  V   L  A  V  T   E  A  W   G  Q  E   A  V  I  P·
331  CCTCAAACCC TGGTCCTCTA TCTGCTGGTC CTGGCAGTCA CTGAAGCCTG GGGCCAGGAG GCAGTCATCC

     ..G  C  H   L  H  P   F  N  V  T   V  R  S   D  R  Q   G  T  C  Q   G  S  H·
421  CAGGCTGCCA CTTGCACCCC TTCAATGTGA CAGTGCGAAG TGACCGCCAA GGCACCTGCC AGGGCTCCCA

     .V  A  Q   A  C  V  G   H  C  E   S  S  A   F  P  S  R   Y  S  V   L  V  A
491  CGTGGCACAG GCCTGTGTGG GCCACTGTGA GTCCAGCGCC TTCCCTTCTC GGTACTCTGT GCTGGTGGCC

      S  G  Y  R   H  N  I   T  S  V   S  Q  C  C   T  I  S   G  L  K   K  V  K  V·
561  AGTGGTTACC GACACAACAT CACCTCCGTC TCTCAGTGCT GCACCATCAG TGGCCTGAAG AAGGTCAAAG
                                        XhoI
                                        ~~~~~~~
          PstI                          SacI  BglII
          ~~~~~~~                       ~~~~~~~~~~~~~
     ..Q  L  Q   C  V  G   S  R  R  E   E  L  E   I  F  T   A  R  A  C   Q  C  D·
631  TACAGCTGCA GTGTGTGGGG AGCCGGAGGG AGGAGCTCGA GATCTTCACG GCCAGGGCCT GCCAGTGTGA
                                     PstI
                                     ~~~~~~
                               EcoRI                 BamHI                 NotI
                               ~~~~~~~               ~~~~~~~               ~~~~~~~
     .M  C  R   L  S  R  Y  (SEQ ID NO: 95)
701  CATGTGTCGC CTCTCTCGCT ACGAATTCCT GCAGCCCGGG GGATCCACTA GTTCTAGAGC GGCCGCCACC (SEQ ID NO: 96)
```

FIG. 28

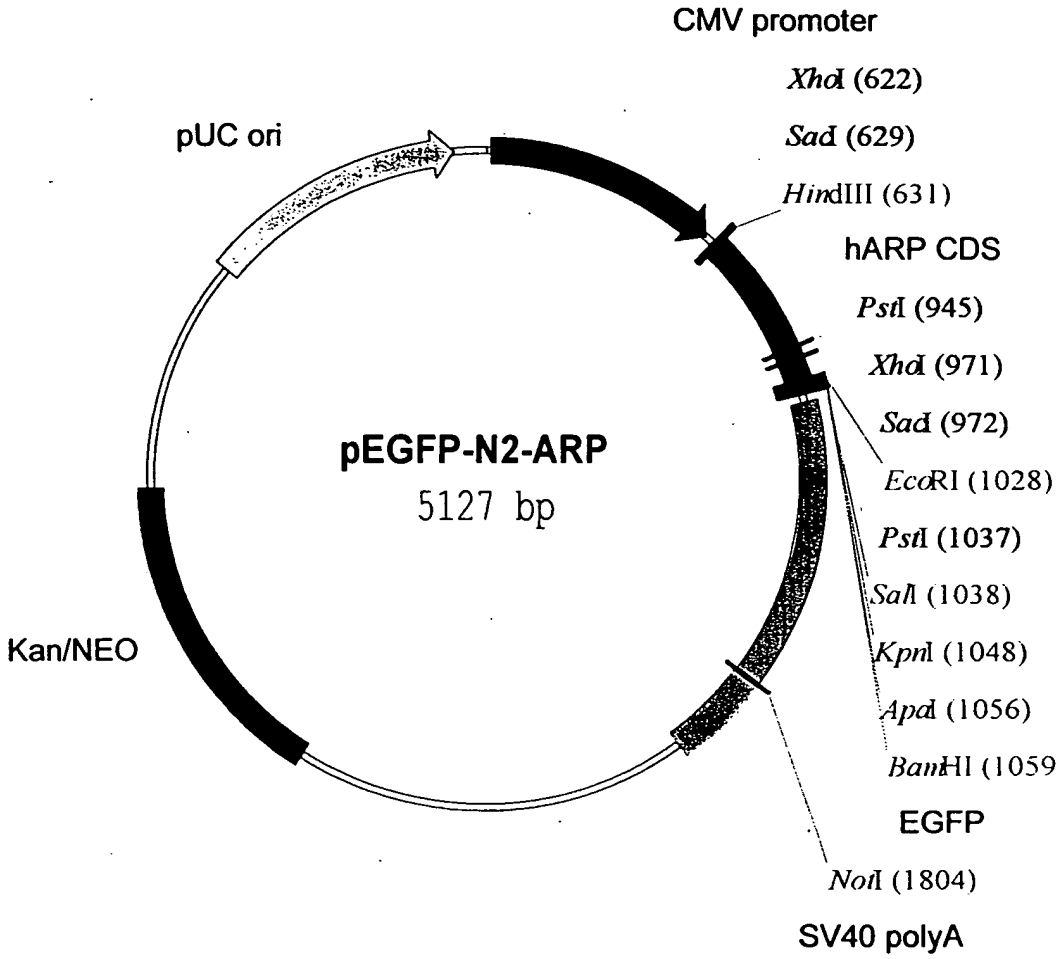

CMV promoter
XhoI (622)
SacI (629)
HindIII (631)
hARP CDS
PstI (945)
XhoI (971)
SacI (972)
EcoRI (1028)
PstI (1037)
SalI (1038)
KpnI (1048)
ApaI (1056)
BamHI (1059
EGFP
NotI (1804)
SV40 polyA
pUC ori
Kan/NEO
pEGFP-N2-ARP
5127 bp

FIG. 29

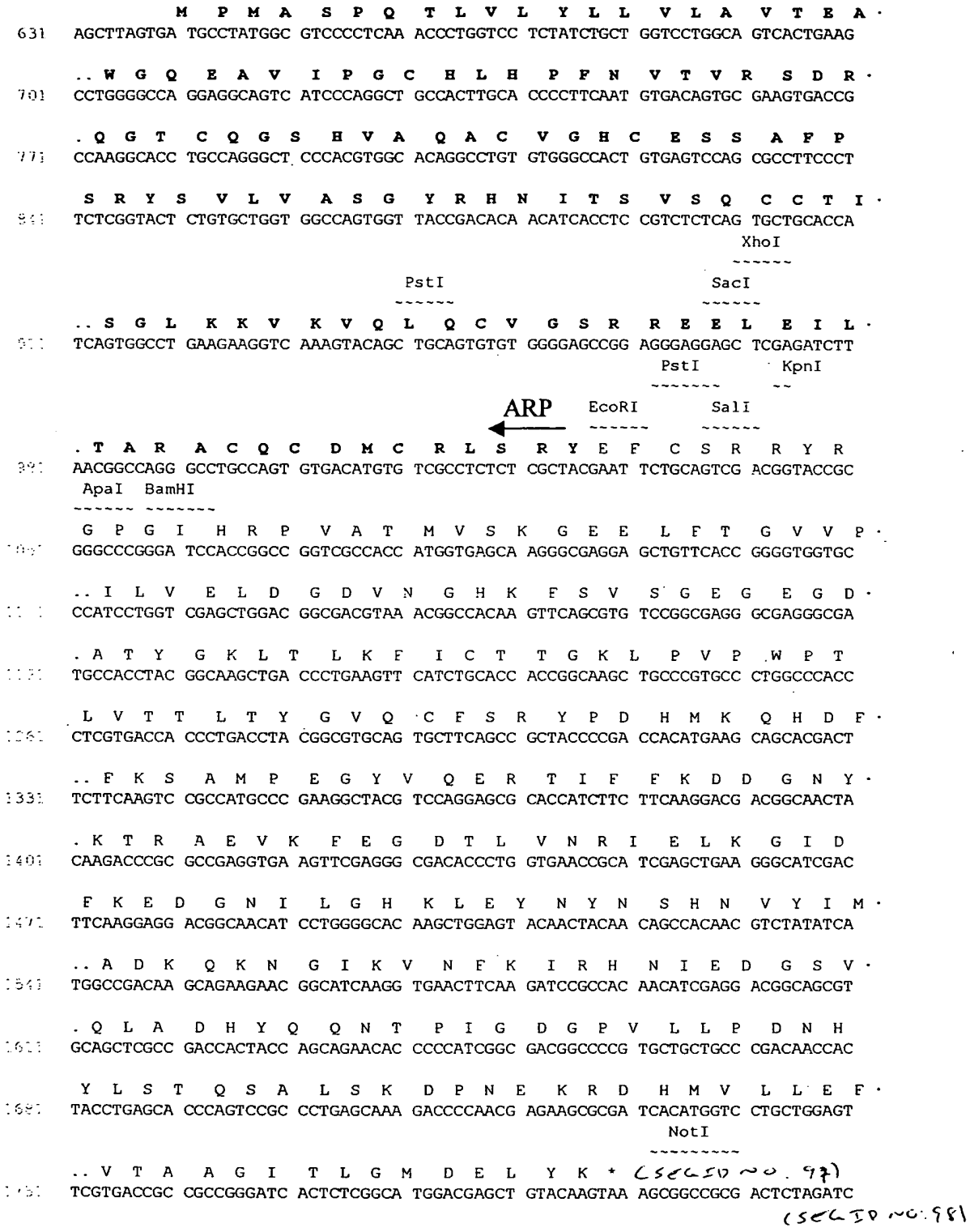
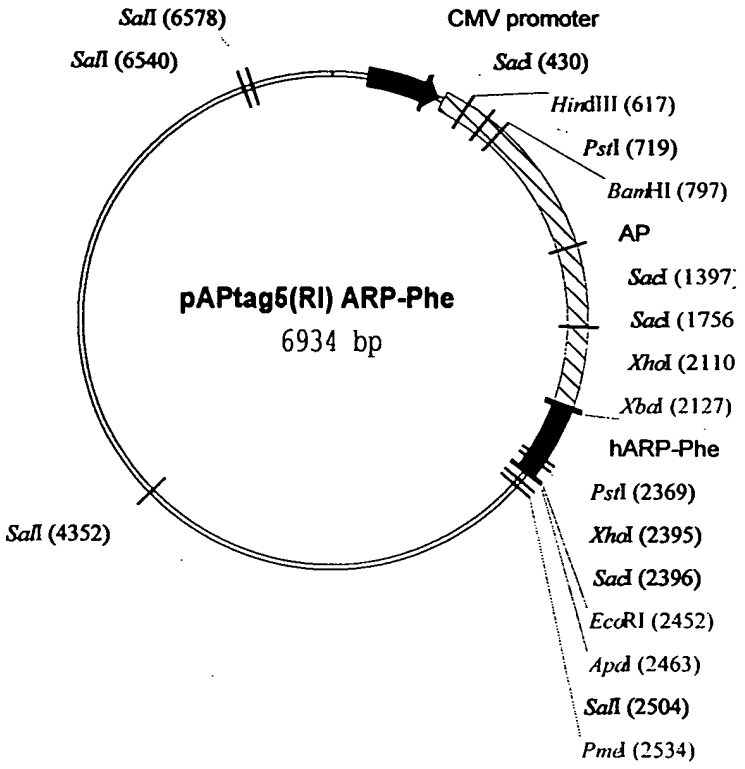

M P M A S P Q T L V L Y L L V L A V T E A
631 AGCTTAGTGA TGCCTATGGC GTCCCCTCAA ACCCTGGTCC TCTATCTGCT GGTCCTGGCA GTCACTGAAG
..W G Q E A V I P G C H L H P F N V T V R S D R
701 CCTGGGGCCA GGAGGCAGTC ATCCCAGGCT GCCACTTGCA CCCCTTCAAT GTGACAGTGC GAAGTGACCG
.Q G T C Q G S H V A Q A C V G H C E S S A F P
771 CCAAGGCACC TGCCAGGGCT CCCACGTGGC ACAGGCCTGT GTGGGCCACT GTGAGTCCAG CGCCTTCCCT
S R Y S V L V A S G Y R H N I T S V S Q C C T I
841 TCTCGGTACT CTGTGCTGGT GGCCAGTGGT TACCGACACA ACATCACCTC CGTCTCTCAG TGCTGCACCA
XhoI
PstI
SacI
..S G L K K V K V Q L Q C V G S R R E E L E I L
911 TCAGTGGCCT GAAGAAGGTC AAAGTACAGC TGCAGTGTGT GGGGAGCCGG AGGGAGGAGC TCGAGATCTT
PstI
KpnI
ARP
EcoRI
SalI
.T A R A C Q C D M C R L S R Y E F C S R R Y R
981 AACGGCCAGG GCCTGCCAGT GTGACATGTG TCGCCTCTCT CGCTACGAAT TCTGCAGTCG ACGGTACCGC
ApaI BamHI
G P G I H R P V A T M V S K G E E L F T G V V P
1051 GGGCCCGGGA TCCACCGGCC GGTCGCCACC ATGGTGAGCA AGGGCGAGGA GCTGTTCACC GGGGTGGTGC
..I L V E L D G D V N G H K F S V S G E G E G D
1121 CCATCCTGGT CGAGCTGGAC GGCGACGTAA ACGGCCACAA GTTCAGCGTG TCCGGCGAGG GCGAGGGCGA
.A T Y G K L T L K F I C T T G K L P V P W P T
1191 TGCCACCTAC GGCAAGCTGA CCCTGAAGTT CATCTGCACC ACCGGCAAGC TGCCCGTGCC CTGGCCCACC
L V T T L T Y G V Q C F S R Y P D H M K Q H D F
1261 CTCGTGACCA CCCTGACCTA CGGCGTGCAG TGCTTCAGCC GCTACCCCGA CCACATGAAG CAGCACGACT
..F K S A M P E G Y V Q E R T I F F K D D G N Y
1331 TCTTCAAGTC CGCCATGCCC GAAGGCTACG TCCAGGAGCG CACCATCTTC TTCAAGGACG ACGGCAACTA
.K T R A E V K F E G D T L V N R I E L K G I D
1401 CAAGACCCGC GCCGAGGTGA AGTTCGAGGG CGACACCCTG GTGAACCGCA TCGAGCTGAA GGGCATCGAC
F K E D G N I L G H K L E Y N Y N S H N V Y I M
1471 TTCAAGGAGG ACGGCAACAT CCTGGGGCAC AAGCTGGAGT ACAACTACAA CAGCCACAAC GTCTATATCA
..A D K Q K N G I K V N F K I R H N I E D G S V
1541 TGGCCGACAA GCAGAAGAAC GGCATCAAGG TGAACTTCAA GATCCGCCAC AACATCGAGG ACGGCAGCGT
.Q L A D H Y Q Q N T P I G D G P V L L P D N H
1611 GCAGCTCGCC GACCACTACC AGCAGAACAC CCCCATCGGC GACGGCCCCG TGCTGCTGCC CGACAACCAC
Y L S T Q S A L S K D P N E K R D H M V L L E F
1681 TACCTGAGCA CCCAGTCCGC CCTGAGCAAA GACCCCAACG AGAAGCGCGA TCACATGGTC CTGCTGGAGT
NotI
..V T A A G I T L G M D E L Y K * (SEQ ID NO. 97)
1751 TCGTGACCGC CGCCGGGATC ACTCTCGGCA TGGACGAGCT GTACAAGTAA AGCGGCCGCG ACTCTAGATC
(SEQ ID NO: 98)

FIG. 30

A.


SalI (6578)
CMV promoter
SalI (6540)
SacI (430)
HindIII (617)
PstI (719)
BamHI (797)
AP
SacI (1397)
SacI (1756
XhoI (2110
XbaI (2127)
hARP-Phe
PstI (2369)
XhoI (2395)
SacI (2396)
EcoRI (2452)
ApaI (2463)
SalI (2504)
PmeI (2534)
pAPtag5(RI) ARP-Phe
6934 bp
SalI (4352)

B.

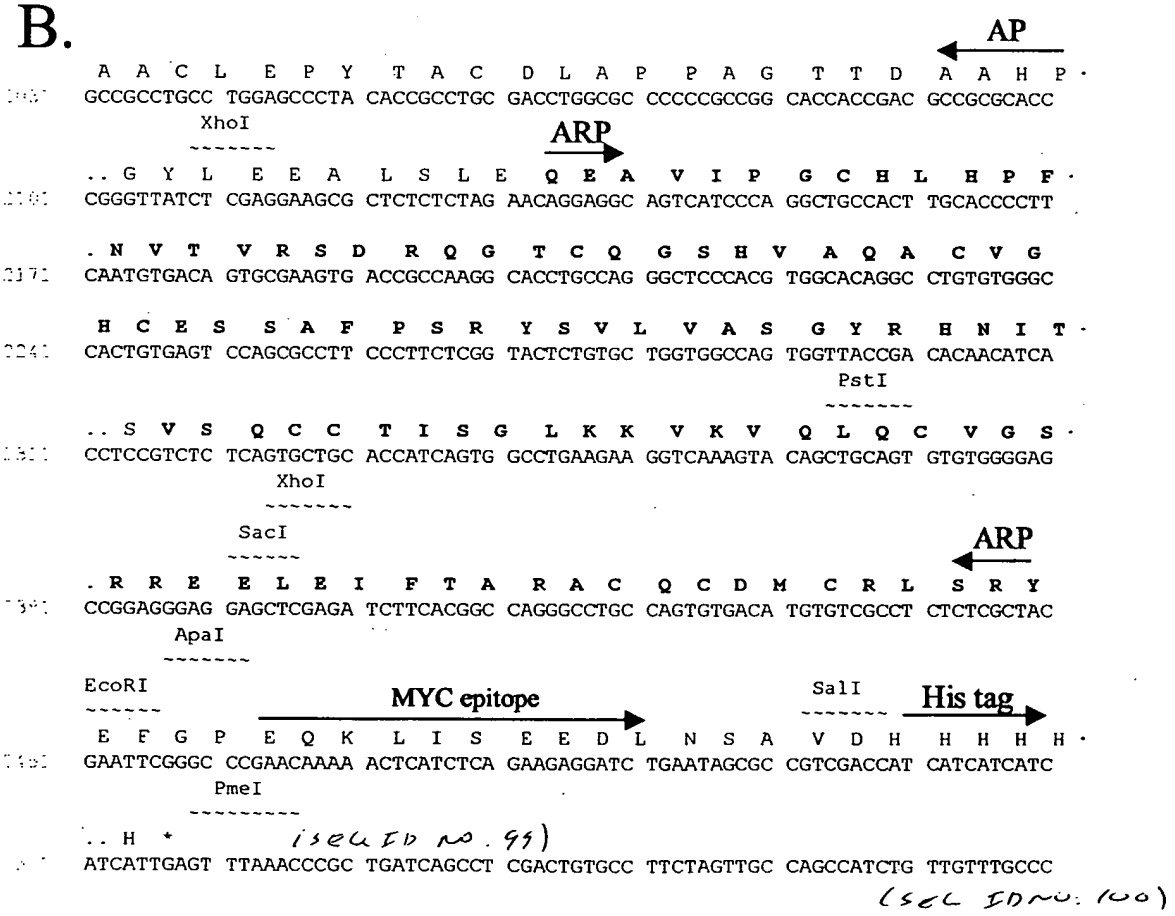
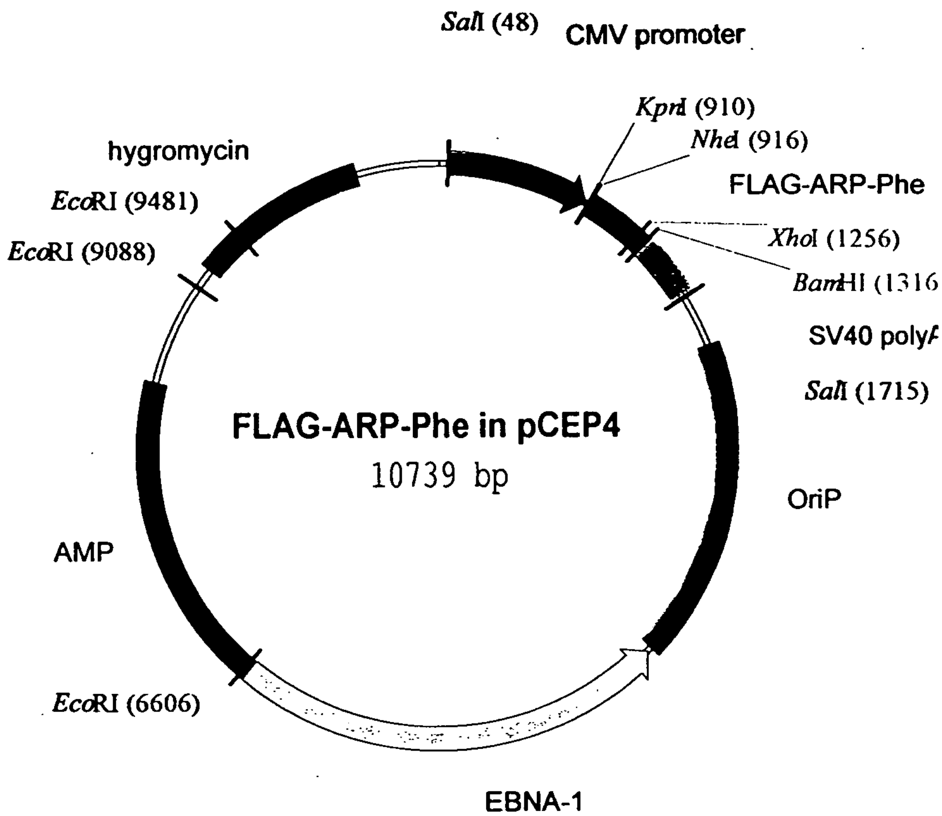

AP
A A C L E P Y T A C D L A P P A G T T D A A H P
GCCGCCTGCC TGGAGCCCTA CACCGCCTGC GACCTGGCGC CCCCCGCCGG CACCACCGAC GCCGCGCACC
XhoI
ARP
G Y L E E A L S L E Q E A V I P G C H L H P F
CGGGTTATCT CGAGGAAGCG CTCTCTCTAG AACAGGAGGC AGTCATCCCA GGCTGCCACT TGCACCCCTT
N V T V R S D R Q G T C Q G S H V A Q A C V G
CAATGTGACA GTGCGAAGTG ACCGCCAAGG CACCTGCCAG GGCTCCCACG TGGCACAGGC CTGTGTGGGC
H C E S S A F P S R Y S V L V A S G Y R H N I T
CACTGTGAGT CCAGCGCCTT CCCTTCTCGG TACTCTGTGC TGGTGGCCAG TGGTTACCGA CACAACATCA
PstI
S V S Q C C T I S G L K K V K V Q L Q C V G S
CCTCCGTCTC TCAGTGCTGC ACCATCAGTG GCCTGAAGAA GGTCAAAGTA CAGCTGCAGT GTGTGGGGAG
XhoI
SacI
ARP
R R E E L E I F T A R A C Q C D M C R L S R Y
CCGGAGGGAG GAGCTCGAGA TCTTCACGGC CAGGGCCTGC CAGTGTGACA TGTGTCGCCT CTCTCGCTAC
ApaI
EcoRI
MYC epitope
SalI
His tag
E F G P E Q K L I S E E D L N S A V D H H H H H
GAATTCGGGC CCGAACAAAA ACTCATCTCA GAAGAGGATC TGAATAGCGC CGTCGACCAT CATCATCATC
PmeI
H *
(SEQ ID NO. 99)
ATCATTGAGT TTAAACCCGC TGATCAGCCT CGACTGTGCC TTCTAGTTGC CAGCCATCTG TTGTTTGCCC
(SEQ ID NO: 100)

FIG. 31

A.



B.

NheI — Mouse preprotrypsin leader → FLAG →

```
                 M  S   A  L  L  I   L  A  L   V  G  A   A  V  A  D   Y  K  D·
911  AGCTGCTAGC CACCATGTCT GCACTTCTGA TCCTAGCTCT TGTTGGAGCT GCAGTTGCTG ACTACAAAGA

              ARP →
    .D  D  D   K  Q  E  A   V  I  P   G  C  H   L  H  P  F   N  V  T   V  R  S
981  CGATGACGAC AAGCAGGAGG CAGTCATCCC AGGCTGCCAC TTGCACCCCT TCAATGTGAC AGTGCGAAGT

     D  R  Q  G   T  C  Q   G  S  H   V  A  Q  A   C  V  G   H  C  E   S  S  A  F·
1051 GACCGCCAAG GCACCTGCCA GGGCTCCCAC GTGGCACAGG CCTGTGTGGG CCACTGTGAG TCCAGCGCCT

    ..P  S  R   Y  S  V   L  V  A  S   G  Y  R   H  N  I   T  S  V  S   Q  C  C·
1121 TCCCTTCTCG GTACTCTGTG CTGGTGGCCA GTGGTTACCG ACACAACATC ACCTCCGTCT CTCAGTGCTG

                                                                       XhoI
    .T  I  S   G  L  K  K   V  K  V   Q  L  Q   C  V  G  S   R  R  E   E  L  E
1191 CACCATCAGT GGCCTGAAGA AGGTCAAAGT ACAGCTGCAG TGTGTGGGGA GCCGGAGGGA GGAGCTCGAG
                                                              BamHI

     I  F  T  A   R  A  C   Q  C  D   M  C  R  L   S  R  Y   *   (SEQ ID NO: 101)
1261 ATCTTCACGG CCAGGGCCTG CCAGTGTGAC ATGTGTCGCC TCTCTCGCTA CTGAGGATCC AGACATGATA
                                                                   (SEQ ID NO: 102)
```

FIG. 32

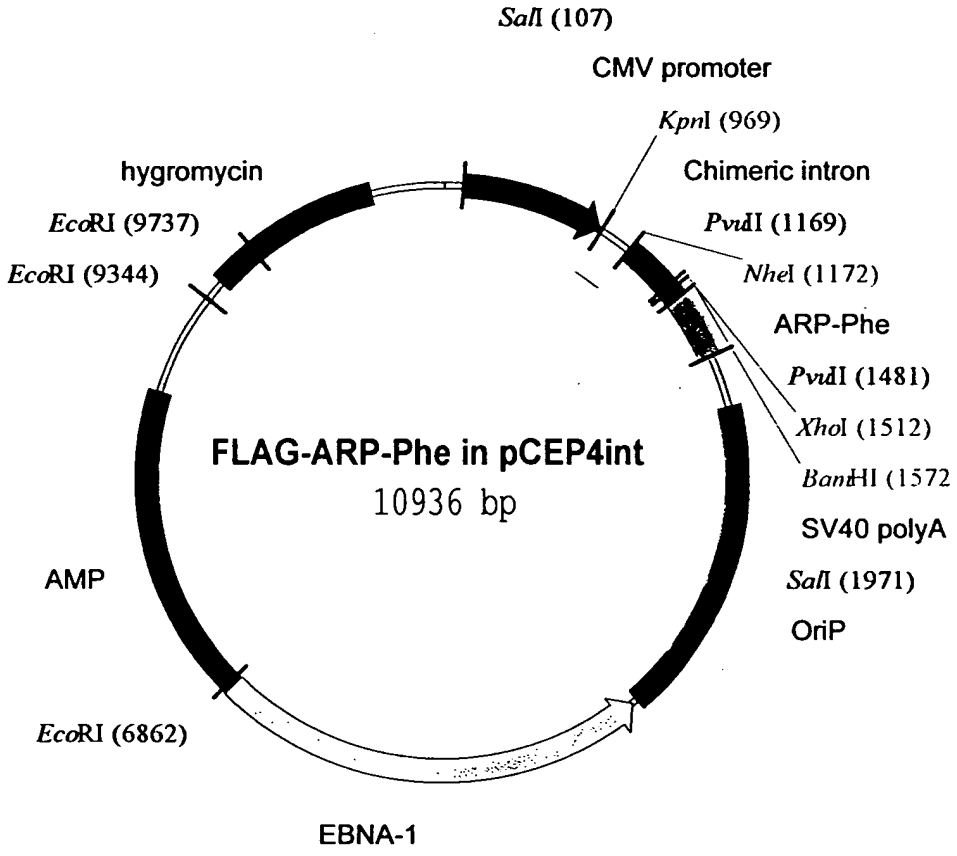
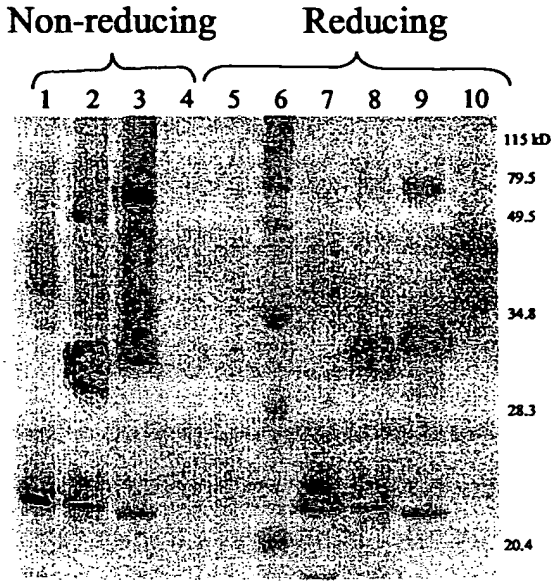

SalI (107)
CMV promoter
KpnI (969)
Chimeric intron
PvuII (1169)
NheI (1172)
ARP-Phe
PvuII (1481)
XhoI (1512)
BamHI (1572
SV40 polyA
SalI (1971)
OriP
EBNA-1
EcoRI (6862)
AMP
EcoRI (9344)
EcoRI (9737)
hygromycin
FLAG-ARP-Phe in pCEP4int
10936 bp

FIG. 33



Lane	Sample
1.	GFP standard (4ng)
2.	BRP-GFP (5 microliters)
3.	ARP-GFP
4.	control transfection (no DNA)
5.	empty
6.	prestained markers
7.	GFP standard (4ng)
8.	BRP-GFP (5 microliters)
9.	ARP-GFP
10.	control transfection (no DNA)

Note – negative controls and ARP-GFP had same total protein load as for 5 microliter sample of BRP-GFP.

FIG. 34

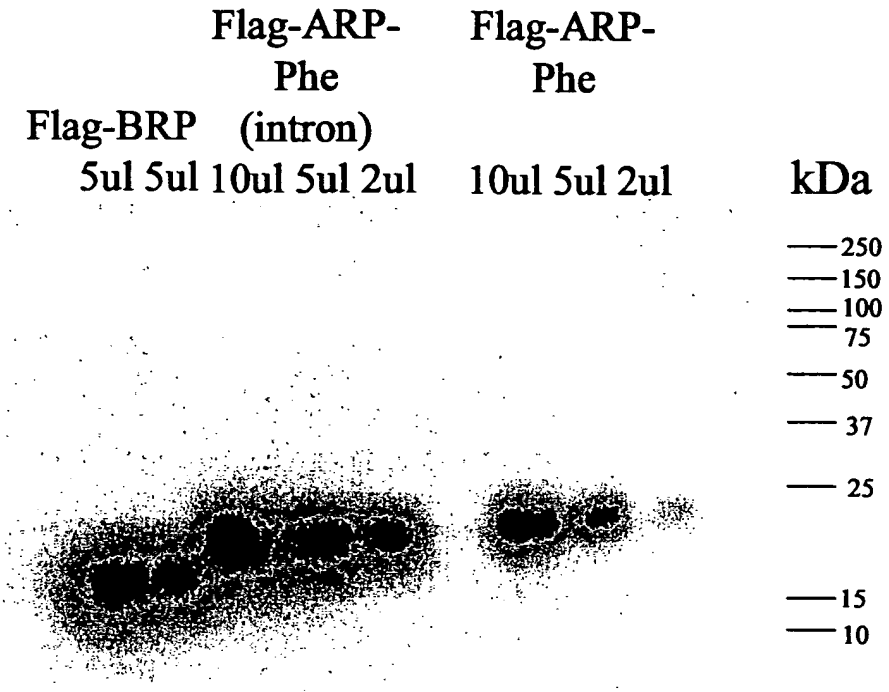
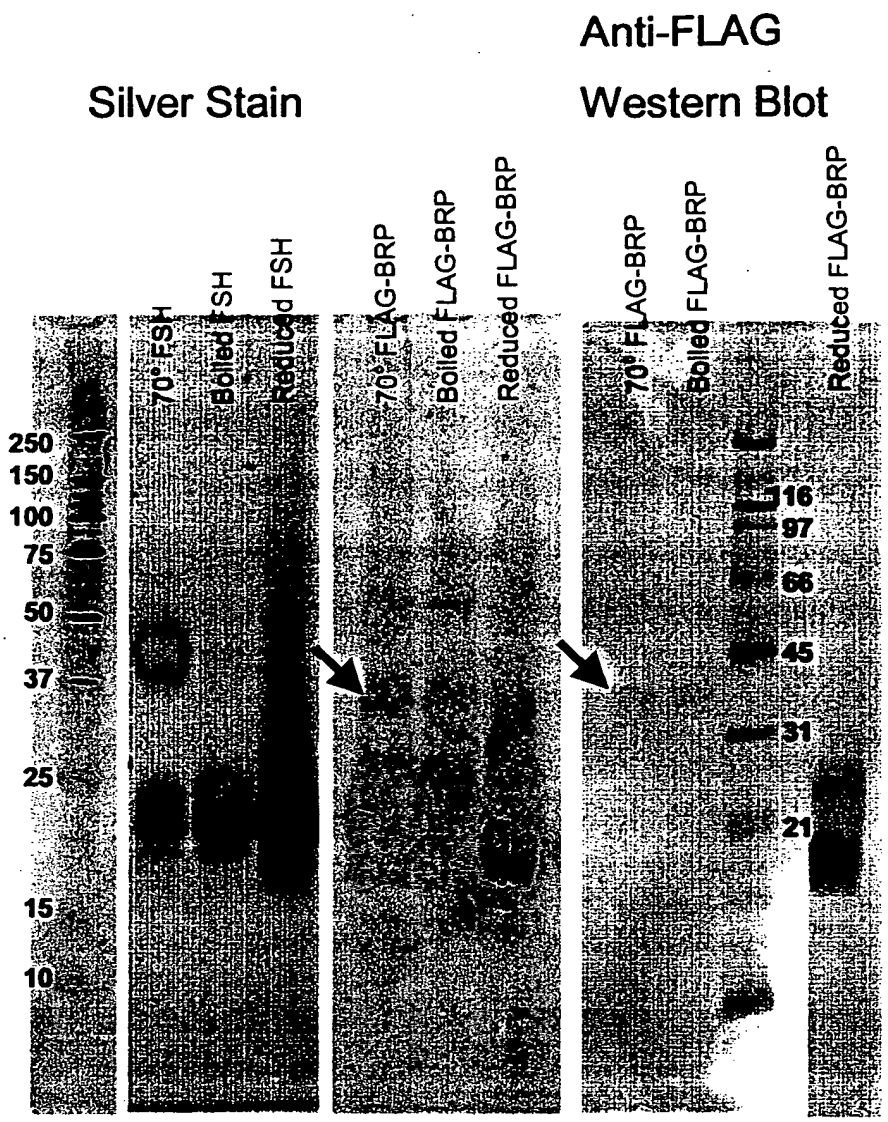

Flag-ARP-
Phe
(intron)
Flag-BRP
5ul 5ul 10ul 5ul 2ul
Flag-ARP-
Phe
10ul 5ul 2ul
kDa
250
150
100
75
50
37
25
15
10

FIG. 35

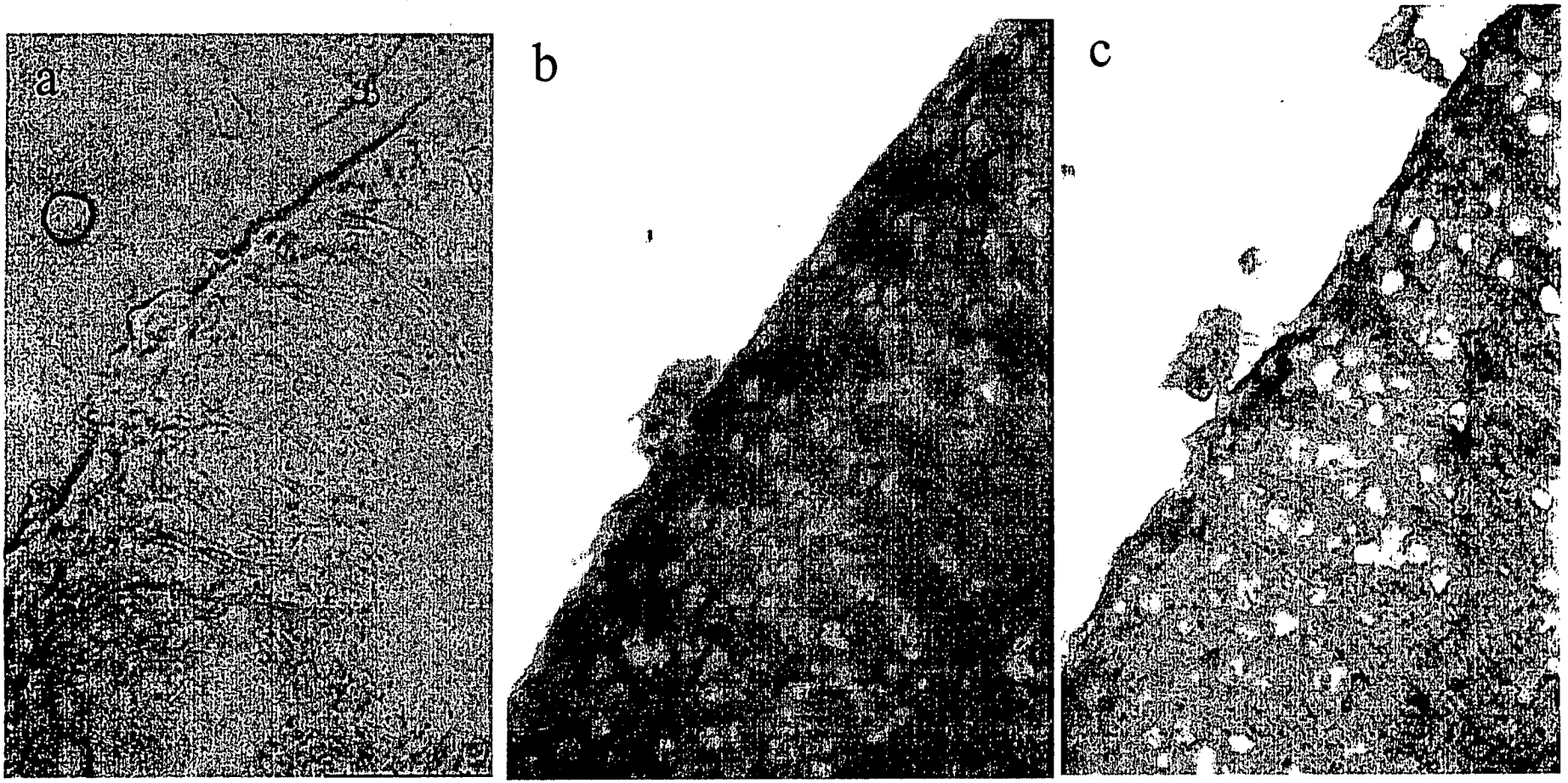


Notes:

- Silver stained (3 left) panels 500 ng loads.
- Western Blots (far right) show 100 ng loads of FLAG-BRP from production lot #2 identified by biotinylated monoclonal anti-FLAG primary antibody and Vector ABC-alkaline phosphatase detection.
- Cyan arrows point to Mr 36 kDa bands which we are interpreting as consistent with disulfide-bonded FLAG-BRP homodimer.

FIG. 36

Fig37. Rat testis

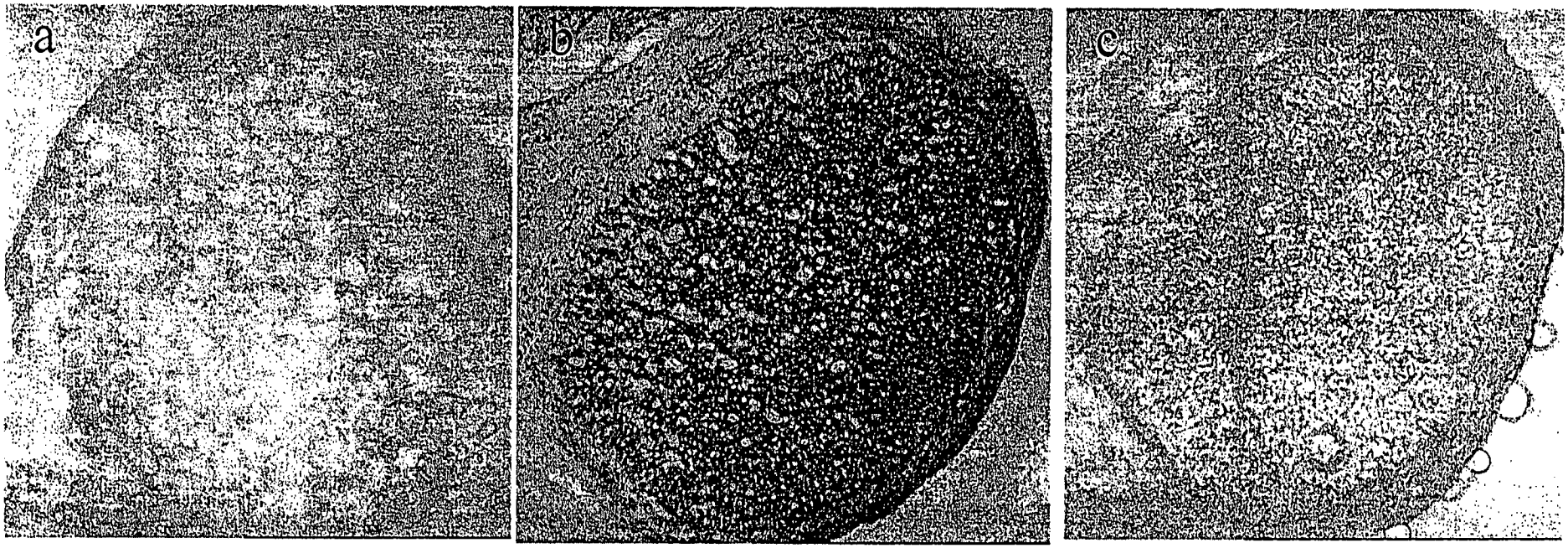


AP

AP-BRP

AP-BRP + FLAG-BRP

Fig 38. Rat ovary

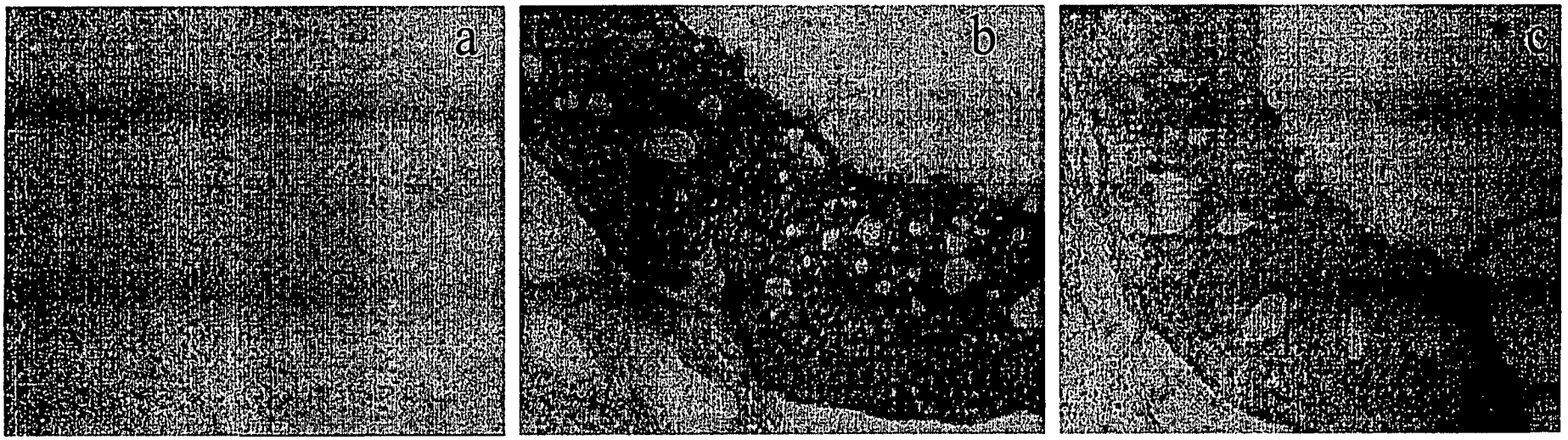


AP

AP-BRP/FLAG-ARP-Phe

AP-BRP/FLAG-ARP-Phe +
FLAG-BRP/His-ARP-Phe

Fig 39. Rat ovary

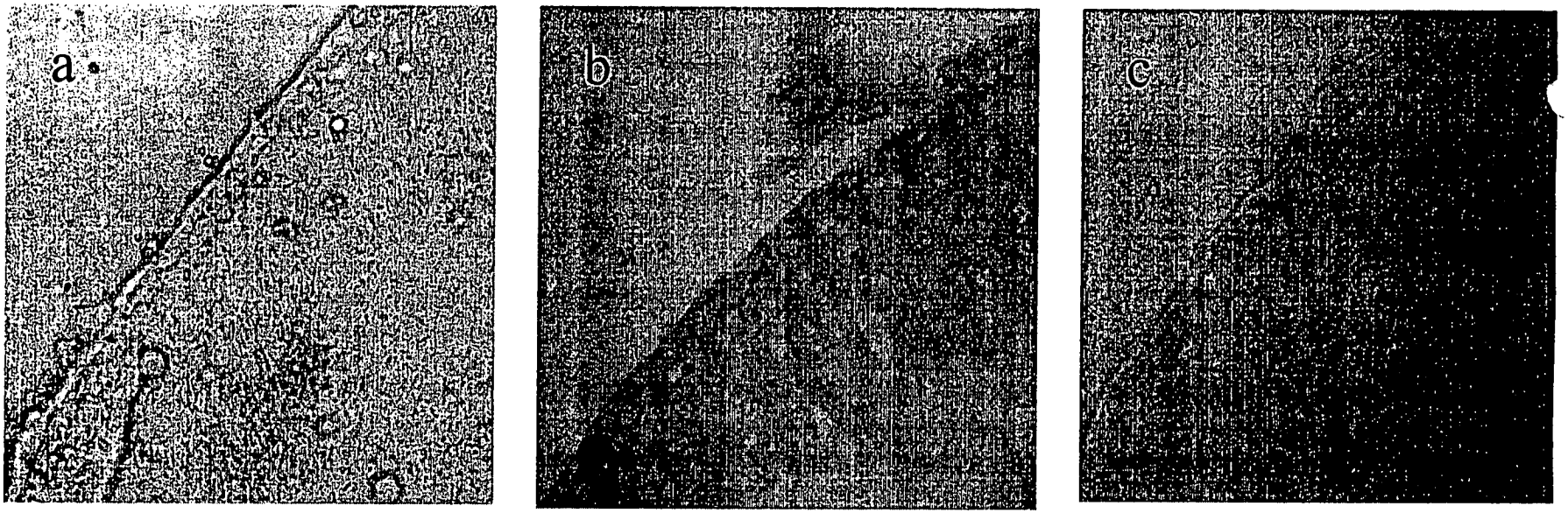


AP

AP-BRP/FLAG-ARP-Phe

AP-BRP/FLAG-ARP-Phe +
FLAG-BRP/His-ARP-Phe

Fig 40. Rat testis

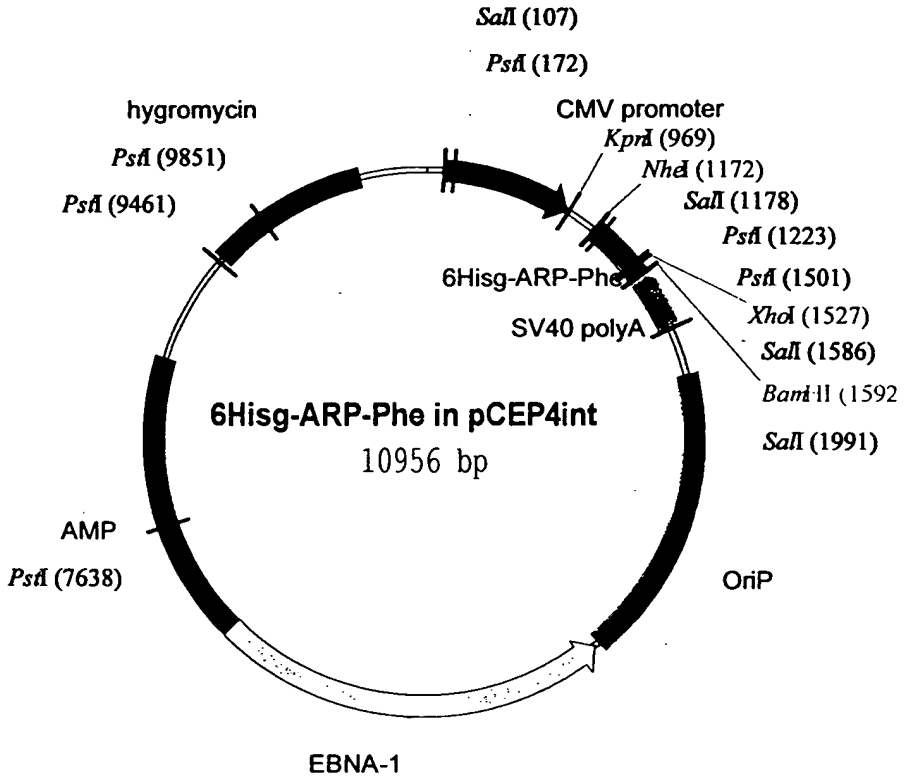


AP

AP-BRP/Flag-ARP-F

AP-BRP/Flag-ARP-F+
FLAG-BRP/His-ARP-Phe

A.


SalI (107)
PstI (172)
hygromycin
CMV promoter
PstI (9851)
KpnI (969)
NheI (1172)
PstI (9461)
SalI (1178)
PstI (1223)
6Hisg-ARP-Phe
PstI (1501)
XhoI (1527)
SV40 polyA
SalI (1586)
BamHI (1592
6Hisg-ARP-Phe in pCEP4int
10956 bp
SalI (1991)
AMP
PstI (7638)
OriP
EBNA-1

B.

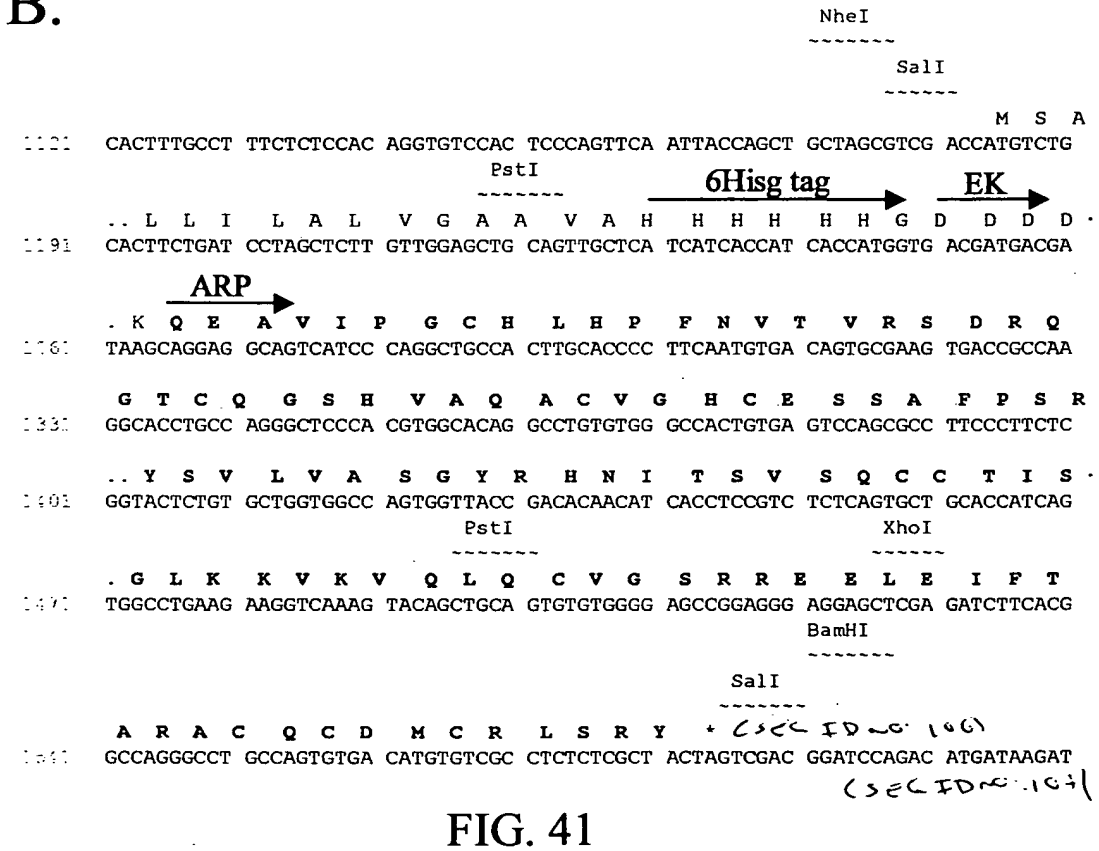

NheI
SalI
M S A
CACTTTGCCT TTCTCTCCAC AGGTGTCCAC TCCCAGTTCA ATTACCAGCT GCTAGCGTCG ACCATGTCTG
PstI
6Hisg tag
EK
.. L L I L A L V G A A V A H H H H H H G D D D D
CACTTCTGAT CCTAGCTCTT GTTGGAGCTG CAGTTGCTCA TCATCACCAT CACCATGGTG ACGATGACGA
ARP
. K Q E A V I P G C H L H P F N V T V R S D R Q
TAAGCAGGAG GCAGTCATCC CAGGCTGCCA CTTGCACCCC TTCAATGTGA CAGTGCGAAG TGACCGCCAA
G T C Q G S H V A Q A C V G H C E S S A F P S R
GGCACCTGCC AGGGCTCCCA CGTGGCACAG GCCTGTGTGG GCCACTGTGA GTCCAGCGCC TTCCCTTCTC
.. Y S V L V A S G Y R H N I T S V S Q C C T I S
GGTACTCTGT GCTGGTGGCC AGTGGTTACC GACACAACAT CACCTCCGTC TCTCAGTGCT GCACCATCAG
PstI
XhoI
. G L K K V K V Q L Q C V G S R R E E L E I F T
TGGCCTGAAG AAGGTCAAAG TACAGCTGCA GTGTGTGGGG AGCCGGAGGG AGGAGCTCGA GATCTTCACG
BamHI
SalI
A R A C Q C D M C R L S R Y * (SEQ ID NO: 106)
GCCAGGGCCT GCCAGTGTGA CATGTGTCGC CTCTCTCGCT ACTAGTCGAC GGATCCAGAC ATGATAAGAT
(SEQ ID NO: 107)

FIG. 41